

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:34:14 ; Search time 46 Seconds
(without alignments)
902.243 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLAALAAASLLHVS.....TIGILMSAPNFVEANSKDF A 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	502	2	US-08-771-737-2
2	2703	100.0	502	2	US-09-954-936-2
3	2698	99.8	502	1	US-08-466-589-8
4	2698	99.8	502	1	US-08-700-636-8
5	2698	99.8	502	2	US-08-467-574-8
6	2698	99.8	502	2	US-09-217-345-8
7	2698	99.8	502	2	US-08-487-596-12
8	2698	99.8	502	2	US-09-892-985-8
9	2698	99.8	502	2	US-09-579-250-2
10	2698	99.8	502	2	US-09-703-951A-12
11	2692	99.6	502	2	US-09-579-250-10
12	2688	99.4	502	2	US-09-579-250-12
13	2682	99.2	502	2	US-09-579-250-14
14	2540	94.0	502	1	US-08-278-635B-7
15	2540	94.0	502	2	US-08-464-258B-7
16	2540	94.0	502	2	US-08-471-961-7
17	2540	94.0	502	2	US-09-345-109C-7
18	2022	74.8	446	2	US-08-660-451A-12
19	1816.5	67.2	511	1	US-08-278-635B-8
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21	1816.5	67.2	511	2	US-08-471-961-8
22	1816.5	67.2	511	2	US-09-345-109C-8
23	1474.5	54.6	470	2	US-09-579-250-6
24	1254.5	46.4	501	2	US-09-303-232C-6
25	1242	45.9	496	2	US-09-303-232C-4
26	1155.5	42.7	770	2	US-09-303-232C-2
27	945	35.0	529	1	US-08-496-855A-2

28	945	35.0	529	2	US-08-487-596-2	Sequence 2, Appli
29	945	35.0	529	2	US-08-660-451A-2	Sequence 2, Appli
30	945	35.0	529	2	US-09-703-951A-2	Sequence 2, Appli
31	943	34.9	510	1	US-08-278-635B-4	Sequence 4, Appli
32	943	34.9	510	2	US-08-471-961-4	Sequence 4, Appli
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37	920.5	34.1	528	1	US-08-700-636-2	Sequence 2, Appli
38	920.5	34.1	528	2	US-08-467-574-2	Sequence 2, Appli
39	920.5	34.1	528	2	US-09-217-345-2	Sequence 2, Appli
40	920.5	34.0	528	2	US-09-892-985-2	Sequence 2, Appli
41	920	34.0	607	2	US-09-949-016-7817	Sequence 7817, Ap
42	916	33.9	627	2	US-08-660-451A-6	Sequence 6, Appli
43	908	33.6	504	1	US-08-466-589-4	Sequence 4, Appli
44	908	33.6	504	1	US-08-700-636-4	Sequence 4, Appli
45	908	33.6	504	2	US-08-467-574-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-771-737-2
; Sequence 2, Application US/08771737
; Patent No. 6323000

; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories

; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

; FILE REFERENCE: 6017.US.01

; CURRENT APPLICATION NUMBER: US/08/771,737

; CURRENT FILING DATE: 1996-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 502

; TYPE: PRT

; ORGANISM: homo sapien

US-08-771-737-2

Query Match 100.0%; Score 2703; DB 2; Length 502;

Best Local Similarity 100.0%; Pred. No. 4.1e-274;

Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	QIMDVDEKNQVLTNTIWLQMS	WDHYLQWNSYSEYGVKTVR	PPDQGIWKPDILLYNSAD	120
QY	121	RFDAFTHTVNLVNSGHCQYL	PPGIFKSSCYDVRFPDVOHCK	LKFGSWSYGGHSLDL	180
DB	121	RFDAFTHTVNLVNSGHCQYL	PPGIFKSSCYDVRFPDVOHCK	LKFGSWSYGGHSLDL	180
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DB	181	QMOEADISGYINGEWDLVGI	PKKSERFEYCKEKPYPDVT	FTVTMRRRTLYYGLNLLIP	240
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QY 301 MIIVGLSVVTVIVLQVHHHDPGGKMPKWKTRVILLNWCAWFLMRKRPGBDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQVHHHDPGGKMPKWKTRVILLNWCAWFLMRKRPGBDKVRPACQHK 360
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Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDDPLAKILEEVRVIANRFRCDSEAVCESEWKEAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDDPLAKILEEVRVIANRFRCDSEAVCESEWKEAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 2
US-09-954-936-2
; Sequence 2, Application US/09954936
; Patent No. 6683157
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A. Murali
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017, US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match 100.0%; Score 2703; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-274;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
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Db 61 QIMDVEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIQWKPDILLYNSADE 120
QY 121 RFDATHTNVLNVSNGHCOYLPFGIKSSCYIDVRWPPDVQHKLKFGSWSYGGWSLDL 180
Db 121 RFDATHTNVLNVSNGHCOYLPFGIKSSCYIDVRWPPDVQHKLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYPNGEWDLVGPKGRSERFECCKEYPDVTFTVTRRRRTLYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGPKGRSERFECCKEYPDVTFTVTRRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300
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Db 301 MIIVGLSVVTVIVLQVHHHDPGGKMPKWKTRVILLNWCAWFLMRKRPGBDKVRPACQHK 360

QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCRLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDDPLAKILEEVRVIANRFRCDSEAVCESEWKEAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDDPLAKILEEVRVIANRFRCDSEAVCESEWKEAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 3
US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-466-589-8
Query Match 99.8%; Score 2698; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIQWKPDILLYNSADE 120
Db 61 QIMDVEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIQWKPDILLYNSADE 120
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Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db 301 MIIVGLSVVTVLVQYHHDDPDGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQHK 360
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Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
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Db 421 LHGGQPEGDPDLAKTILEEVRYIANRFRCDSEAVCEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-08-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5916582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen B.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-700-636-8

Query Match 99.8%; Score 2698; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273; Indels 0; Gaps 0;
Matches 501; Conservative 0; Mismatches 1;
Qy 1 MRCSPGVWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGVWLAALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKQVLTNNIWLQMSWTQHYLQNVNVEYPOKTVRPPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNNIWLQMSWTQHYLQNVNVEYPOKTVRPPDGOIWKPDILLYNSADE 120
Qy 121 RFDAFHTNVLNSSGHCOYLPGIFKSSCYIDVRWPPFDVQHCCKLKFGSWSYGGSLDL 180
Db 121 RFDAFHTNVLNSSGHCOYLPGIFKSSCYIDVRWPPFDVQHCCKLKFGSWSYGGSLDL 180
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Db 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECKEKPYPDVFTVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db 301 MIIVGLSVVTVLVQYHHDDPDGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPEGDPDLAKTILEEVRYIANRFRCDSEAVCEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKTILEEVRYIANRFRCDSEAVCEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-467-574-8

Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
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DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAST 300
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DB 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
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RESULT 6

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US-09-217-345-8
; Sequence 8, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAnuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA

```

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; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-217-345-8

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Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKLVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGGWSLDL 180
DB 121 RFDAFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVDTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVDTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
DB 301 MIIVGLSVVTVTVLYQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
QY 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
DB 361 QRCRSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFAACVVDRCLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502

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Db 481 ICTIGILMSAPNFVEAVSKDFA 502
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RESULT 7
US-08-487-596-12
; Sequence 12, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-596-12
Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNTIWLQSWTDHYLQWNVSEYGVKTVRFDGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTIWLQSWTDHYLQWNVSEYGVKTVRFDGQIWKPDILLYNSADE 120
QY 121 RPDATHTTNVNLNSSGHCQYLPPIFKSCYIDVRWFPDVOHQCKLKPGSWSYGGHSLDL 180
Db 121 RPDATHTTNVNLNSSGHCQYLPPIFKSCYIDVRWFPDVOHQCKLKPGSWSYGGHSLDL 180
QY 181 QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLLPADSGEKISLITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLLPADSGEKISLITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWRVILLNWCANFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWRVILLNWCANFLMRKPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKILEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 8
US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-JUN-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:		Best Local Similarity 99.8%; Pred. No. 1.4e-273;		Best Local Similarity 99.8%; Pred. No. 1.4e-273;		
SEQUENCE CHARACTERISTICS:		LENGTH: 502 amino acids		Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
TYPE: amino acid		STRANDEDNESS: single				
TOPOLOGY: unknown						
MOLECULE TYPE: protein						
SEQUENCE DESCRIPTION: SEQ ID NO: 8:						
US-09-892-985-8						
Query Match		99.8%; Score 2698; DB 2; Length 502;				
Best Local Similarity 99.8%; Pred. No. 1.4e-273;						
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
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DB	1	MRCSPGGWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTVYFSLSLL 60		DB	1	MRCSPGGWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTVYFSLSLL 60
QY	61	QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRPPDGGQIWKPDILLYNSADE 120		QY	61	QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRPPDGGQIWKPDILLYNSADE 120
DB	61	QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRPPDGGQIWKPDILLYNSADE 120		DB	61	QIMDVEKNQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRPPDGGQIWKPDILLYNSADE 120
QY	121	RFDATFTNTLVNNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180		QY	121	RFDATFTNTLVNNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
DB	121	RFDATFTNTLVNNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180		DB	121	RFDATFTNTLVNNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSL 180
QY	181	QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTVMRRRTLYYGLNLLIP 240		QY	181	QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTVMRRRTLYYGLNLLIP 240
DB	181	QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTVMRRRTLYYGLNLLIP 240		DB	181	QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFVTVMRRRTLYYGLNLLIP 240
QY	241	CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300		QY	241	CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB	241	CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300		DB	241	CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY	301	MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360		QY	301	MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
DB	301	MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360		DB	301	MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVPACQHK 360
QY	361	QRCRSIASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420		QY	361	QRCRSIASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
DB	361	QRCRSIASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420		DB	361	QRCRSIASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY	421	LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480		QY	421	LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
DB	421	LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480		DB	421	LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY	481	ICTIGILMSAPNFVEAVSKDFA 502		QY	481	ICTIGILMSAPNFVEAVSKDFA 502
DB	481	ICTIGILMSAPNFVEAVSKDFA 502		DB	481	ICTIGILMSAPNFVEAVSKDFA 502
RESULT 9		US-09-579-250-2		US-09-703-951A-12		
SEQUENCE 2, Application US/09579250				SEQUENCE 12, Application US/09703951A		
PATENT NO. 6693172				PATENT NO. 6936457		
GENERAL INFORMATION:				GENERAL INFORMATION:		
APPLICANT: Groppi, Vincent				APPLICANT: Gillespie, Alison		
APPLICANT: Wolfe, Mark L.				Claeps, Brian O.		
APPLICANT: Berkenpas, Mitchell B				Chavez-No. 6936457iega, Laura Elena		
TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel				Siegel, Robert		
FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists				Elliot, Kathryn J.		
CURRENT FILING DATE: 2000-05-25				TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS		
NUMBER OF SEQ ID NOS: 14				OF NEURONAL NICOTINIC ACETYLCHOLINE		
SOFTWARE: PatentIn Ver. 2.1				RECEPTOR, CELLS TRANSFORMED THEREWITH,		
SEQ ID NO 2				AND RECOMBINANT CELL LINE EXPRESSING		
LENGTH: 502				NUMBER OF SEQUENCES: 18		
TYPE: PRT				CORRESPONDENCE ADDRESS:		
ORGANISM: Homo sapiens				ADDRESSEE: Merck & Co., Inc.		
US-09-579-250-2				STREET: 126 E. Lincoln Avenue		
				CITY: Rahway		
				STATE: NJ		
				COUNTRY: USA		
				ZIP: 07065-0907		
				COMPUTER READABLE FORM:		
				MEDIUM TYPE: Floppy disk		
				COMPUTER: IBM PC compatible		
				OPERATING SYSTEM: PC-DOS/MS-DOS		
				SOFTWARE: PatentIn Release #1.0, Version #1.25		
				CURRENT APPLICATION DATA:		
				APPLICATION NUMBER: US/09/703,951A		
				FILING DATE: 01-No. 6936457-2000		
				CLASSIFICATION: <unknown>		
				PRIOR APPLICATION DATA:		
				APPLICATION NUMBER: US 08/487,596		

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;
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-703-951A-12

Query Match          99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.4e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGWMLAASLLHVSLSQGFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWMLAASLLHVSLSQGFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFTNVLNVSNGHCQYLPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Db 121 RFDATFTNVLNVSNGHCQYLPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Db 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQ 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQ 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12
US-09-579-250-12
; Sequence 12, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12

Query Match          99.6%; Score 2692; DB 2; Length 502;
Best Local Similarity 99.6%; Pred. No. 5.8e-273;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRCSPGGWMLAASLLHVSLSQGFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWMLAASLLHVSLSQGFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFTNVLNVSNGHCQYLPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Db 121 RFDATFTNVLNVSNGHCQYLPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
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Db 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYF 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQ 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPBGDKVRPACQ 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12
US-09-579-250-12
; Sequence 12, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
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[illegible]


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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7

* Query Match          94.0%; Score 2540; DB 1; Length 502;
  Best Local Similarity 93.6%; Pred. No. 4.9e-257; Indels 0; Gaps 0;
  Matches 465; Conservative 18; Mismatches 14;

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-258B-7

Query Match          94.0%; Score 2540; DB 2; Length 502;
Best Local Similarity 93.6%; Pred. No. 4.9e-257; Indels 0; Gaps 0;
Matches 465; Conservative 18; Mismatches 14;

QY      6 GGWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
DB      6 GGWLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
QY      66 DEKNQVLTNNIWLQMSWTDHYLQWNSYEPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
DB      66 DEKNQVLTNNIWLQMSWTDHYLQWNSYEPGVKTVRFPDQGIWKPDIILYNSADERFDT 125
QY      126 FHTNVLNAGHCQYLPPIGIFKSSCYIDVRWFFDVQHCKLFGSWSYGGWSLDLQWQEA 185
DB      126 FHTNVLNAGHCQYLPPIGIFKSSCYIDVRWFFDVQHCKLFGSWSYGGWSLDLQWQEA 185
QY      126 FHTNVLNAGHCQYLPPIGIFKSSCYIDVRWFFDVQHCKLFGSWSYGGWSLDLQWQEA 185
DB      126 FHTNVLNAGHCQYLPPIGIFKSSCYIDVRWFFDVQHCKLFGSWSYGGWSLDLQWQEA 185
QY      186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTVTMMRRRTLYYGLNLLIPCVLIS 245
DB      186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTVTMMRRRTLYYGLNLLIPCVLIS 245
QY      186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTVTMMRRRTLYYGLNLLIPCVLIS 245
DB      186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTVTMMRRRTLYYGLNLLIPCVLIS 245
QY      246 ALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASVTIIG 305
DB      246 ALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASVTIIG 305
QY      306 LSVVTVIVLYHHDDPDGGMKPKWTRVILLNWCWFLMRKRGEDKVRPACQHKORRCS 365
DB      306 LSVVTVIVLYHHDDPDGGMKPKWTRVILLNWCWFLMRKRGEDKVRPACQHKORRCS 365
QY      366 LASVMSAVAPPPASNGNLLYIGFGLDGVHCVPTPDGSGVCGMACSPTHDHLHGQ 425
DB      366 LASVMSAVAPPPASNGNLLYIGFGLDGVHCVPTPDGSGVCGMACSPTHDHLHGQ 425
QY      366 LASVELSAGAGPTSGNLLYIGFGLGHCACAPTDPGSGVCGRLACSPTHDHLHGHAH 425
DB      366 LASVELSAGAGPTSGNLLYIGFGLGHCACAPTDPGSGVCGRLACSPTHDHLHGHAH 425
QY      426 PPGDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFVSFTIITIG 485
DB      426 PPGDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFVSFTIITIG 485
QY      486 ILMSAPNFVEAVSKDPA 502
DB      486 ILMSAPNFVEAVSKDPA 502

Search completed: March 28, 2006, 13:35:35
Job time : 47 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:26:24 ; Search time 188 seconds
(without alignments)
1173.235 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLAAALHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Genesecp1980s:*
2: Genesecp1990s:*
3: Genesecp2000s:*
4: Genesecp2001s:*
5: Genesecp2002s:*
6: Genesecp2003as:*
7: Genesecp2003bs:*
8: Genesecp2004s:*
9: Genesecp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	2	AAW69216
2	2698	99.8	502	2	AAW44153
3	2698	99.8	502	2	AAW09025
4	2698	99.8	502	3	AAW24088
5	2698	99.8	502	4	AAW82690
6	2698	99.8	502	4	AAW50012
7	2698	99.8	502	5	ABG70492
8	2698	99.8	502	5	ABW82435
9	2698	99.8	502	7	ADA10874
10	2698	99.8	502	7	ADA47051
11	2698	99.8	502	7	ADE57310
12	2698	99.8	502	7	ADM68431
13	2698	99.8	502	9	AEW90709
14	2698	99.8	515	9	AEC01800
15	2693	99.6	502	8	ADE52166
16	2692	99.6	502	4	AAW50015
17	2690	99.5	502	7	ADK52598
18	2690	99.5	502	8	ADSL7052
19	2690	99.5	502	8	ADR88593
20	2688	99.4	502	4	AAW50016
21	2682	99.2	502	4	AAW50017
22	2675	99.0	502	8	ADR47549
23	2675	99.0	502	8	ADR47553
24	2675	99.0	502	9	AEW90713

25	2670	98.8	502	8	ADW52189	Adw52189 Rhesus mo
26	2670	98.8	502	8	ADR47551	ADR47551 Rhesus mo
27	2547	94.2	502	9	AEW90707	AEW90707 Rat alpha
28	2546	94.2	502	9	AEW90711	AEW90711 Mouse alp
29	2543	94.1	502	9	AEW90722	AEW90722 Rat alpha
30	2542	94.0	502	8	ADW52172	ADW52172 Rat alpha
31	2536	93.8	499	9	AEW90715	AEW90715 Bos tauru
32	2531	93.6	502	7	ADW57308	ADW57308 Rat Prote
33	2531	93.6	502	7	ADW47049	ADW47049 Rat Prote
34	2522.5	93.3	531	8	ADR15995	ADR15995 Splice va
35	2429	89.9	502	2	AAW12368	AAW12368 Neuronal
36	2429	89.9	502	9	AEW90717	AEW90717 Chicken a
37	2073.5	76.7	509	9	AEW90719	AEW90719 Zebra fis
38	2022	74.8	446	7	ADA10865	ADA10865 Human neu
39	2018	74.7	446	7	ADM68422	ADM68422 Human nic
40	1816.5	67.2	511	2	AAW12369	AAW12369 Neuronal
41	1790	66.2	349	5	ABP69081	ABP69081 Human pol
42	1474.5	54.6	470	4	AAW50014	AAW50014 Chimeric
43	1360.5	50.3	448	4	AAW50018	AAW50018 Mature ce
44	1344	49.7	246	9	AEW19062	AEW19062 Human nic
45	1254.5	46.4	501	3	AAW50816	AAW50816 H. viresc

ALIGNMENTS

RESULT 1

AAW69216

ID AAW69216 standard; protein; 502 AA.

XX AAW69216;

XX AAW69216;

DT 09-OCT-1998 (first entry)

DE V274T variant human alpha7 nAChR protein.

XX Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;

KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;

KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;

KW schizophrenia.

XX Homo sapiens.

XX WO9828331-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US023405.

XX 20-DEC-1996; 96US-00771737.

XX (ABBO) ABBOTT LAB.

XX Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM, Roch J;

PI Sullivan JP, Touma E;

XX WPI; 1998-377593/32.

DR N-PSDB; AAW44687.

XX Nucleic acid encoding variant of human alpha 7 nicotinic acetylcholine

PT receptor sub-unit - used to identify modulators of the receptor,

PT potentially useful for treating neuro-degeneration, cancer etc.

XX Claim 15; Fig 2; 44pp; English.

XX This sequence is the V247T variant of human alpha7 nicotinic

CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing

CC the DNA are used to express the protein and to identify modulators of

CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds

CC or antagonists that are potentially useful for treating

CC neurodegeneration, enzyme dysfunction, affective disorders and immune

CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic

CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,

CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridization or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
CC retained
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 2703; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 7e-263;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSCYIDVRWPFDPVQHCXKFKGWSYGGWSL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSCYIDVRWPFDPVQHCXKFKGWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEPYPDVTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEPYPDVTFTVTRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVTVLQYHHDDPGGKVPKWTTRVILLNWCWFLMRKRGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLQYHHDDPGGKVPKWTTRVILLNWCWFLMRKRGEDKVRPACQHK 360

QY 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPEGDPDLAKLILEEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKLILEEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFEAVSKDFA 502
DB 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 2
AAW44153
ID AAW44153 standard; protein; 502 AA.
XX AC AAW44153;
XX XX
DT 14-MAY-1998 (first entry)
XX
DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACHR; antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT 229..256
FT /label= TMD1
FT /note= "transmembrane domain"
FT

FT Domain 262..284
FT /label= TMD2
FT /note= "transmembrane domain"
FT Domain 290..317
FT /label= TMD3
FT /note= "transmembrane domain"
FT Domain 318..461
FT /label= cytoplasmic_loop
FT Misc-difference 343
FT /note= "encoded by CTS"
FT 462..487
FT /label= TMD4
FT /note= "transmembrane domain"
XX
PN W09420617-A2.
XX
PD 15-SEP-1994.
XX
PF 08-MAR-1994; 94WO-US002447.
XX
PR 08-MAR-1993; 93US-00028031.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Elliott KJ, Ellis SB, Harpold MM;
XX
DR WPI; 1994-303024/37.
DR N-PSDB; AAV12197.
XX
PT Human neuronal nicotinic acetylcholine receptor subunits and DNA - also
PT transformed cells useful for screening cpds. which modulate activity of
XX the receptor.
XX
PS Claim 7; Page 80-81; 99pp; English.
XX
CC The present sequence represents a human neuronal nicotinic acetylcholine
CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
CC NACHR subunits may be used in a method of screening compounds to identify
CC any which modulate the activity of human neuronal NACHR. Subunit specific
CC antibodies may be used to monitor the distribution and expression density
CC of various subunits in normal vs diseased brain tissues. Testing of
CC single receptor subunits or specific receptor subunit combinations with a
CC variety of potential agonists or antagonists provides information with
CC respect to the function and activity of the individual subunits and
CC should lead to the identification and design of compounds that are
CC capable of very specific interaction with one or more receptor subtypes.
CC The resulting drugs should exhibit fewer unwanted side effects than drugs
CC identified e.g. screening with cells that express a variety of subtypes
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSCYIDVRWPFDPVQHCXKFKGWSYGGWSL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGFKSCYIDVRWPFDPVQHCXKFKGWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEPYPDVTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEPYPDVTFTVTRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
AAW09025
ID AAW09025 standard; protein; 502 AA.
XX
AC AAW09025;
DT 09-APR-1997 (first entry)
XX
DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX
KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW ligand-gated receptor.
XX
OS Homo sapiens.
XX
PN WO9641876-A1.
XX
PD 27-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009775.
XX
PR 07-JUN-1995; 95US-00484722.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Harpold MM;
XX
DR WPI; 1997-065463/06.
DR N-PSDB; AAT48239.
XX
PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
PT in screening to determine the effect of drugs on the receptor.
XX
PS Disclosure; Page 73-74; 108pp; English.
XX
CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
CC acetylcholine receptor (nAChR) can be expressed in transformed host cells
CC carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp.
CC mammalian cells or amphibian oocytes, expressing the recombinant alpha-7
CC subunit, opt. in combination with other recombinant alpha and/or beta
CC subunits (see also AAW09018-24, AAW09026-27), can be used to examine the
CC function of human AChR and to identify cpds. that modulate its activity
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGVWLAALASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTITNWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTITNWLQMSWTDHYLQWNVSEYFGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSNWYGGWSL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSNWYGGWSL 180
QY 181 QMQEADISGYIPNGSMDLVGIPKESERFYECKEPPYDVTFTVMRRRTLYVGLNLLIP 240
Db 181 QMQEADISGYIPNGSMDLVGIPKESERFYECKEPPYDVTFTVMRRRTLYVGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
AAB24088
ID AAB24088 standard; protein; 502 AA.
XX
AC AAB24088;
DT 29-JAN-2001 (first entry)
XX
DE Human PRO2145 protein sequence SEQ ID NO:77.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoeleic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000376.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037F.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX

DR	WPI; 2000-572270/53.	
XX	N-PSDB; AAC58395.	
PT	Thirty PRO polynucleotides encoding PRO polypeptides, useful in the	
XX	treatment, diagnosis and prevention of cancer.	
PS	Claim 61; Fig 58; 286pp; English.	
XX	The present invention describes an isolated antibody that binds to one of	
CC	the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,	
CC	PRO1717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,	
CC	PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,	
CC	PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR	
CC	PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The	
CC	PRO polypeptides and nucleotides are useful in the treatment, diagnosis	
CC	and prevention of cancer. The antibodies and other anti-tumour compounds	
CC	may be used to treat various conditions, including those characterised by	
CC	overexpression and/or activation of the amplified PRO genes. Exemplary	
CC	conditions or disorders to be treated with such antibodies and other	
CC	compounds include benign or malignant tumours (e.g., renal, liver,	
CC	kidney, bladder, breast, gastric, ovarian, colorectal, prostate,	
CC	pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,	
CC	glioblastomas, and various head and neck tumours), leukaemias and	
CC	astrocytic malignancies, other disorders such as neuronal, glial,	
CC	lymphoid malignancies, and other glandular, macrophagal, epithelial,	
CC	stromal and blastocoealic disorders, and inflammatory, angiogenic and	
CC	immunologic disorders. AAC58242 to AAC58366 represent PCR primers and	
CC	hybridisation probes used in the isolation of the human PRO sequences.	
CC	AAC58367 to AAC58396 and AAC24057 to AAC24089 represent human PRO	
CC	polynucleotide and protein sequences given in the exemplification of the	
CC	present invention	
XX	Sequence 502 AA;	
SQ		
Query Match		
Best Local Similarity 99.8%; Score 2698; DB 3; Length 502;		
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 MRCSPGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVDNSOPLTVYFSLSL 60	
Db	1 MRCSPGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVDNSOPLTVYFSLSL 60	
QY	61 QIMDVDEKNQVLTNIIWLQMSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADE 120	
Db	61 QIMDVDEKNQVLTNIIWLQMSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADE 120	
QY	121 RFDATHTNVLVNSGHCQYLPPGIPKSSCYIDVRWFPDPVOHCKLKFGSWSYGGWSLDL 180	
Db	121 RFDATHTNVLVNSGHCQYLPPGIPKSSCYIDVRWFPDPVOHCKLKFGSWSYGGWSLDL 180	
QY	181 QMOEADISGYIPNGEWDLVGIPKGSERFEYCKEPYDPVTFVTVMRRRTLYYGLNLLIP 240	
Db	181 QMOEADISGYIPNGEWDLVGIPKGSERFEYCKEPYDPVTFVTVMRRRTLYYGLNLLIP 240	
QY	241 CVLISALALLVFLPADSGEKISLGTITVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300	
Db	241 CVLISALALLVFLPADSGEKISLGTITVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300	
QY	301 MIIVGLSVVVTVIQLYHHHDPGGKMPKWTTRVILLNWCWFLRMKRPGEOKVRPACQHK 360	
Db	301 MIIVGLSVVVTVIQLYHHHDPGGKMPKWTTRVILLNWCWFLRMKRPGEOKVRPACQHK 360	
QY	361 QRCSLASVEMENAVPPASNGNLIYIGRGLDGVHCVTPDPSGVCCGMACTHDEHL 420	
Db	361 QRCSLASVEMENAVPPASNGNLIYIGRGLDGVHCVTPDPSGVCCGMACTHDEHL 420	
QY	421 LHGGQPPGDPDLAKLLEEVRIYANFRQDSEAVCSWEKFAACVVDRLCLMAFSVF 480	
Db	421 LHGGQPPGDPDLAKLLEEVRIYANFRQDSEAVCSWEKFAACVVDRLCLMAFSVF 480	
QY	481 ICTIGILMSAPNFVEAVSKDPA 502	
Db	481 ICTIGILMSAPNFVEAVSKDPA 502	

RESULT 5	
AA82690	
ID	AA82690 standard; protein; 502 AA.
XX	
AC	AA82690;
XX	
DT	15-OCT-2001 (first entry)
XX	
DE	Nicotinic acetylcholine receptor alpha7.
XX	
KW	Nicotinic acetylcholine receptor; nAChR; human;
KW	acetylcholine binding protein; AChBP; mollusc; ligand-binding protein;
KW	ligand-gated ion channel; crystal; drug design; protein co-ordinate data;
KW	schizophrenia; Alzheimer's disease; nicotine addiction;
KW	Tourette's syndrome; therapy; nootropic; neuroprotective.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	108..115
FT	/note= "conserved ligand-binding region, residues Trp108
FT	and Tyr115 are essential"
FT	171..173
FT	/note= "conserved ligand-binding region, residues Trp171
FT	and Tyr173 are essential"
FT	210..217
FT	/note= "conserved ligand-binding region, residues Tyr210,
FT	Cys212, Cys213 and Tyr217 are essential"
XX	
PN	WO200158951-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-EP001457.
XX	
PR	10-FEB-2000; 2000EP-00200443.
PR	31-OCT-2000; 2000EP-00203810.
XX	
PA	(TEWE-) STICHTING TECH WETENSCHAPPEN.
XX	
PI	Smit AB, Sixma TK;
XX	
DR	WPI; 2001-497071/54.
XX	
PT	Water-soluble ligand-binding proteins derived from molluscs and analogs
PT	of ligand-gated ion channels, useful in drug screening assay, where the
PT	drugs identified can be used in the treatment of Alzheimer's disease or
PT	schizophrenia.
XX	
PS	Disclosure; Page 252-254; 260pp; English.
XX	
CC	The present sequence is that of the alpha subunit of human nicotinic
CC	acetylcholine receptor (nAChR). The sequence includes regions that are
CC	conserved throughout the various nAChR alpha subunits and which are
CC	essential for ligand binding. The invention relates to water-soluble
CC	ligand-binding proteins derived from molluscs, especially acetylcholine-
CC	binding proteins (AChBPs) and analogues of ligand-gated ion channels,
CC	their crystals, and their use for screening ligands of ligand-gated ion
CC	channels. The water-soluble ligand-binding proteins are capable of
CC	forming multimers and are amenable to crystallization. The crystal
CC	structure of AChBP is provided, and can be used to generate 3D models of
CC	the extracellular ligand-binding domain of ligand-gated ion channels and
CC	thus for screening of drugs that act on these ion channels. Chimeric
CC	proteins are provided that are capable of binding a ligand of a ligand-
CC	gated receptor, and comprise at least the amino acids of the AChBP
CC	determining solubility of the AChBP, in the same positions as in the
CC	AChBP, and also comprising amino acids determining binding to the ligand.
CC	In the chimeric proteins, at least the essential amino acids of at least
CC	1 of the conserved regions of an nAChR have been substituted for the
CC	corresponding amino acids, and preferably entire stretches have been
CC	substituted. New drugs can be developed that selectively intervene in

CC neuronal signalling pathways, especially where the ligand-gated ion
CC channel is the nAChR, and the related disorder is Tourette's syndrome,
CC Alzheimer's disease, addiction to nicotine or schizophrenia
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGIWKPDILLYNSADE 120
QY 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWLSLDL 180
DB 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWLSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDPVTVTWMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDPVTVTWMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
AAB50012
XX AAB50012 standard; protein; 502 AA.
XX
XX AAB50012;
XX
XX
XX 14-MAR-2001 (first entry)
XX
DE Wild-type human alpha7 ligand gated ion channel.
XX
XX Human; alpha7 nicotinic acetylcholine gated ion channel;
XX Human; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
XX
XX Homo sapiens.
XX
XX WO200073431-A2.
XX
XX
XX 07-DEC-2000.
XX
XX 25-MAY-2000; 2000WO-US011862.
XX
XX 27-MAY-1999; 99US-0136174P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Groppi VE, Wolfe ML, Berkenpas MB;

XX WPI; 2001-061524/07.
DR N-PSDB; AAC90380.
XX
PT Special cell culture medium for treating cells and for inducing mammalian
cell lines to conduct calcium ions, comprising specified concentrations
of ions of sodium, calcium and potassium at specified pH.
XX
XX Disclosure; Page 61-63; 77pp; English.
XX
CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the cells
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGIWKPDILLYNSADE 120
QY 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWLSLDL 180
DB 121 RPDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFPDVOHCKLKFGSWSGWLSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDPVTVTWMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDPVTVTWMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
ABG70492
ID ABG70492 standard; protein; 502 AA.
XX
XX AC ABG70492;
XX
XX DT 06-DEC-2002 (first entry)
XX
XX Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
XX Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
XX ion flux; alpha 7 subunit.
XX

OS Homo sapiens.
PN US6440681-B1.
XX
XX
PD 27-AUG-2002.
XX
XX 07-JUN-1995; 95US-00487596.
XX
PR 03-APR-1990; 90US-00504455.
PR 20-NOV-1992; 92US-00938154.
PR 08-MAR-1993; 93US-00028031.
PR 08-NOV-1993; 93US-00149503.
XX
XX (MERI) MERCK & CO INC.
XX
XX Elliott KJ, Ellis SB, Harpold MM;
PI WPI; 2002-711528/77.
DR N-PSDB; ABS54875.
XX
XX Identifying antagonists or agonists of human neuronal nicotinic
PT acetylcholine receptors, by contacting recombinant cells with test
PT compound, and measuring ion flux of cells or binding of compound to
PT nNACHR.
XX
XX Claim 101; Col 59-64; 56pp; English.
XX
XX The invention relates to a method for identifying compounds that are
CC antagonists or agonists of human neuronal nicotinic acetylcholine
CC receptors (nNACHR), by contacting recombinant cells with a test compound
CC and measuring ion flux, the electrophysiological response of the cells or
CC binding of the test compound to the nNACHR. The recombinant cells are
CC produced by transfection with a nucleic acid encoding at least one human
CC nNACHR (alpha or beta) subunit, such that the cells express an nNACHR
CC comprising one human subunit encoded by the transfected nucleic acid.
CC This sequence represents the alpha 7 subunit of the human nNACHR
XX polypeptide
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFORLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFORLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60

QY 61 QIMDVDEKNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120

QY 121 RFDATFHTNVLVNSGHCQYLPPIPKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDL 180
DB 121 RFDATFHTNVLVNSGHCQYLPPIPKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDL 180

QY 181 OMQEADISGVINGEWDLVGIPKRSERFVECKEYPDVTFTVTRRTLYYGNLLIP 240
DB 181 OMQEADISGVINGEWDLVGIPKRSERFVECKEYPDVTFTVTRRTLYYGNLLIP 240

QY 241 CVLISALALLVFPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPIAQYFAST 300
DB 241 CVLISALALLVFPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPIAQYFAST 300

QY 301 MIIVGLSVVTVIVLYHHDDPGGQPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYHHDDPGGQPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360

QY 361 QRCSLASVEMSAVAPPASGNLLYIGRGDGVHCVPTPDGCVVCGRMACSPTHDEHL 420
DB 361 QRCSLASVEMSAVAPPASGNLLYIGRGDGVHCVPTPDGCVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILLEEVRYIANRFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480

DB 421 LHGGQPPEGDPDLAKILLEEVRYIANRFRQDSEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 8
ABB82435
ID ABB82435 standard; protein; 502 AA.
XX
XX ABB82435;
XX
XX 22-JAN-2003 (first entry)
XX
XX Human neuronal NACHR alpha7 subunit.
XX
XX Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
KW immunochemistry; NACHR alpha7 subunit; receptor.
XX
XX Homo sapiens.
OS
XX
XX WO200259266-A2.
XX
XX 01-AUG-2002.
XX
XX 29-OCT-2001; 2001WO-US050985.
XX
XX 01-NOV-2000; 2000US-00703951.
XX
XX (MERI) MERCK & CO INC.
XX
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
PI WPI; 2002-698532/75.
DR N-PSDB; ABV73248.
XX
XX Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro screening
PT of a drug substance in a test system specific for humans.
XX
XX Example; Page 130-131; 143pp; English.
XX
XX The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHR alpha7 subunit
XX
XX Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFORLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAASLLHVSLOGEFORLYKELVKNYNPLERPVPANDSQPLTVYFSLSL 60

QY 61 QIMDVDEKNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120

QY 121 RFDATFHTNVLVNSGHCQYLPPIPKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDL 180
DB 121 RFDATFHTNVLVNSGHCQYLPPIPKSSCYIDVRWFFDVQHCCLKFGSWYGGWSLDL 180

Db 121 RPDATFHTNVLNNSGHCQYLPPIGPKSSCYIDVRWFPDQVQCKLKFSGWSYSGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTVMRRRTLYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTVMRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300
QY 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPCEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPCEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDSSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDSSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 9
ADA10874
ID ADA10874 standard; protein; 502 AA.
XX AC ADA10874;
XX DT 06-NOV-2003 (first entry)
XX DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1.
XX KW alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor;
XX KW ligand-gated ion channel; synaptic transmission; gene therapy;
XX KW transgenic; receptor.
XX OS Homo sapiens.
XX PN US6524789-B1.
XX PD 25-FEB-2003.
XX PF 07-JUN-1996; 96US-00660451.
XX PR 07-JUN-1995; 95US-00484722.
XX PA (MERI) MERCK & CO INC.
XX PI Elliott KJ, Harpold MM;
XX WPI; 2003-511917/48.
XX DR N-PSDB; ADA10864.
XX PT New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human
XX PT neuronal nicotinic acetylcholine receptor (nAChR); useful for identifying
XX PT compounds that modulate human neuronal nAChR activity.
XX PS Disclosure; Col 67-72; 63pp; English.
XX CC The invention relates to an isolated nucleic acid molecule comprising a
XX CC nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human
XX CC neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligand-
XX CC gated ion channels that mediate synaptic transmissions between nerve and
XX CC muscle and between neurons upon interaction with the neurotransmitter
XX CC acetylcholine. The nucleic acid molecule is useful for identifying
XX CC compounds that modulate human neuronal nAChR. The present sequence
XX CC represents the amino acid sequence of the human neuronal nicotinic
XX CC acetylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present

CC sequence is the sequence encoded by the nAChR alpha 7 subunit DNA
CC ADA10864.
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 7; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAAGLLHVSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSPGGVWLAALAAAGLLHVSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNWLQMSWTDHYLQWNVSEYFGVKTVPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNWLQMSWTDHYLQWNVSEYFGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RPDATFHTNVLNNSGHCQYLPPIGPKSSCYIDVRWFPDQVQCKLKFSGWSYSGWSL 180
Db 121 RPDATFHTNVLNNSGHCQYLPPIGPKSSCYIDVRWFPDQVQCKLKFSGWSYSGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTVMRRRTLYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTVMRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTIVLLSTTFMLLVAEIMPATSDSVPLIAQVFAST 300
QY 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPCEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLYQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPCEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPTDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDSSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDSSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 10
ADA10851
ID ADD47051 standard; protein; 502 AA.
XX AC ADD47051;
XX DT 02-DEC-2004 (revised)
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein NP_000737, SEQ ID NO 12739.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX OS Unidentified.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; NP_000737.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
PS Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 7; Length 502;
Best Local Similarity 99.8%; Pred. No. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAASLLHVSLQGEFQKLYKELVKXNPNLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSLQGEFQKLYKELVKXNPNLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYFGVKTVRPDQGIWKPDILLVNSADE 120
DB 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYFGVKTVRPDQGIWKPDILLVNSADE 120
QY 121 RFDATFHTNVLVNSSGHCOYLPPIGFKSSCYIDVRWFPDVQCHLKFQSWSYGWSGLDL 180
DB 121 RFDATFHTNVLVNSSGHCOYLPPIGFKSSCYIDVRWFPDVQCHLKFQSWSYGWSGLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERYECKEPYDPDVTVTVMRRRTLYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERYECKEPYDPDVTVTVMRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTIVLLNWCWFLRKPCGEDKVRPACQHK 360
DB 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTIVLLNWCWFLRKPCGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420

DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGGDDPLAKILREVRVIANRFRQDESEAVCSWKFAACVDRLCCLMAFSVFTI 480
DB 421 LHGGOPPEGGDDPLAKILREVRVIANRFRQDESEAVCSWKFAACVDRLCCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 11
ADES7310
ID ADES7310 standard; protein; 502 AA.
XX ADES7310;
AC ADES7310;
XX 29-JAN-2004 (first entry)
DT Human Protein P36544, SEQ ID NO 3171.
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P36544.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 7; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGIWKPDILLYNSADE 120
 QY 121 RFDATFHTNVLNVSNGHCQYLPPIGPKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
 DB 121 RFDATFHTNVLNVSNGHCQYLPPIGPKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGECKVRPACQHK 360
 DB 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGECKVRPACQHK 360
 QY 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 DB 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12

ID ADM68431
 AC ADM68431 standard; protein; 502 AA.

AC ADM68431;

AC ADM68431;

DT 03-JUN-2004 (first entry)

XX Human nicotinic acetylcholine receptor alpha 7 subunit #2.

XX Human; neuronal nicotinic acetylcholine receptor; alpha subunit;
 KW receptor; nAChR; neuronal disorder; Alzheimer's disease.

XX Homo sapiens.

XX US2003138911-A1.

XX 24-JUL-2003.

XX 23-JAN-2003; 2003US-00349836.

XX 07-JUN-1995; 95US-00484722.

XX 07-JUN-1996; 96US-00660451.

XX

PA (MERI) MERCK & CO INC.

PI Elliott KJ, Harpold MM;

XX WPI; 2003-851732/79.

DR N-PSDB; ADM68421.

XX New nucleic acid molecule, useful for preparing a composition for

PT diagnosing or treating neuronal disorders, e.g. Alzheimer's disease.

XX Disclosure; Page 35-37; 57pp; English.

PS The invention relates to an isolated nucleic acid molecule comprising a
 CC sequence of nucleotides encoding an alpha 6 or beta 3 subunit of a human
 CC neuronal nicotinic acetylcholine receptor (nAChR). Also included are
 CC isolating DNA encoding a human nicotinic acetylcholine receptor subunit,
 CC cells (comprising a nucleic acid molecule where the cells are prokaryotic
 CC cells or eukaryotic cells and the nucleic acid is heterologous to the
 CC cell) and identifying functional neuronal nicotinic acetylcholine
 CC receptor subunits and their combinations. The nucleic acid molecule is
 CC useful for preparing a composition for diagnosing or treating neuronal
 CC disorders, e.g. Alzheimer's disease. The present sequence represents a
 CC nAChR alpha subunit. NOTE: The present sequence is encoded by ADM68421
 CC but differs from the sequence appearing as ADM68422.

XX Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 7; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.2e-262;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 DB 1 MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDGIWKPDILLYNSADE 120
 QY 121 RFDATFHTNVLNVSNGHCQYLPPIGPKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
 DB 121 RFDATFHTNVLNVSNGHCQYLPPIGPKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEPYDVTFTVWRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGECKVRPACQHK 360
 DB 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGECKVRPACQHK 360
 QY 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 DB 361 QRCRLASVEMSAVAPPASNGNLLYIGRGLDGHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 13

AEB90709
 ID AEB90709 standard; protein; 502 AA.

XX AEB90709;

AC AEB90709;

XX 06-OCT-2005 (first entry)
DT Human alpha 7 nAChR wild-type protein SeqID7.
DE protein purification; acetylcholine; Nicotinic ACh; neuroprotective;
KW gene therapy; neurodegenerative disease; mood disorder; immune disorder.
XX Homo sapiens.
XX US2005170360-A1.
XX 04-AUG-2005.
XX 30-JAN-2004; 2004US-00769085.
XX 30-JAN-2004; 2004US-00769085.
XX (PAPK/) PAPKE R L.
XX (PLAC/) PLACZEK A.
XX Papke RL, Placzek A;
XX WPI; 2005-562714/57.
DR N-PSDB; AEB90708.
XX Novel isolated variant alpha 7 nicotinic acetylcholine receptor
PT polypeptide having second transmembrane domain comprising serine residue
PT in sixth amino acid position, useful for treating neurological
PT conditions.
XX Disclosure; SEQ ID NO 7; 89pp; English.
XX This invention relates to a novel isolated variant alpha 7 nicotinic
XX acetylcholine receptor (nAChR) polypeptide having a second transmembrane
XX (TM2) domain comprising a serine residue in the sixth amino acid
XX position. The invention may be useful for the development of compounds
XX with a neuroprotective activity whilst the disclosed sequence may prove
XX useful for gene therapy. The invention is useful for treating conditions
XX associated with neurodegenerative processes, enzymatic function,
XX affective disorders or immuno function. The present sequence is that of a
XX wild-type nAChR protein which was used during the isolation of the novel
XX variant nAChR alpha-7 receptors of the invention.
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 9; Length 502;
Best Local Similarity 99.8%; Pred. NO. 2.2e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIMKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIMKPDILLYNSADE 120
QY 121 RPDATHTNVLNNSGHCQYLPFGICFSCYIDVRFPDVOHCKLKFGSWSYGWSL 180
DB 121 RPDATHTNVLNNSGHCQYLPFGICFSCYIDVRFPDVOHCKLKFGSWSYGWSL 180
QY 181 QMQEADISGYPNGEVDLVPKRSERFVECKEYPDPVTFVTWRRRTLYGLNLLIP 240
DB 181 QMQEADISGYPNGEVDLVPKRSERFVECKEYPDPVTFVTWRRRTLYGLNLLIP 240
QY 241 CVLISALLVFLLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALLVFLLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTIVLYQHHHDPDGGQMPKWTIVLLNWCWFLBMRKPGEDKVRPACQHK 360
DB 301 MIIVGLSVVVTIVLYQHHHDPDGGQMPKWTIVLLNWCWFLBMRKPGEDKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDDPDLAKLLEEVRYIANFRQDSEAVCSEWKEAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDDPDLAKLLEEVRYIANFRQDSEAVCSEWKEAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 14
AEC01800
ID AEC01800 standard; protein; 515 AA.
XX AEC01800;
AC AEC01800;
XX 20-OCT-2005 (first entry)
DT Alpha-7 nicotinic receptor with HSV tag.
XX Alpha-7 nicotinic receptor with HSV tag.
DE Gastrointestinal-Gen.; Antiinflammatory; Antiulcer; Antipsoriatic;
KW Neuroprotective; Antirheumatic; Antiarthritic; Hemostatic; Antidiabetic;
KW Antiasthmatic; Antiallergic; Dermatological; Ophthalmological;
KW Cytostatic; Anti-HIV; Virucide; Antibacterial; Tuberculostatic;
KW Fungicide; Antiparkinsonian; Nootropic; Serotonin-Reuptake-Inhibitor;
KW INPIONCHI; 5-HT3 receptor; chromosome 17q25.1; T cell.
XX Homo sapiens.
OS Synthetic.
OS WO2005073251-A1.
PN 11-AUG-2005.
PD 28-JAN-2005; 2005WO-GB000292.
XX 28-JAN-2004; 2004GB-00001882.
PR (INPH-) INPHARMATICA LTD.
XX Lobley AE, Michalovich D, Stancovski I, Allen KE, Allen JM;
PI Osypenko VN, Gurney AM;
XX WPI; 2005-555693/56.
DR Treating diseases associated with T cells, such as inflammatory bowel
PT diseases, multiple sclerosis, psoriasis, arthritis, diabetes, asthma and
PT Alzheimer's disease, by administering a 5-HT3 receptor protein or
PT encoding nucleic acid.
XX Example 7; Page 73; 122pp; English.
PS This sequence represents the protein alpha-7 nicotinic receptor with HSV
XX tag at the C terminal. Alpha-7 nicotinic receptor is homologous to
CC INPIONCHI which is a non-selective cation channel which is predicted to
CC contain four transmembrane domains and a signal peptide of 23 amino
CC acids. It functions as a member of the 5-HT3 receptor group, preferably
CC as a 5-HT3 receptor subunit. INPIONCHI is a 421 amino acid protein
CC encoded by 9 exons located on human chromosome 17q25.1. INPIONCHI has
CC been cloned from human thymus and it is expressed on mammalian cell
CC surface membranes. It is closely related to a murine 5-HT3-b receptor
CC subunit. INPIONCHI is used in the method of the invention for treating a
CC disease associated with T cells in a patient. The method comprises
CC administering to the patient an INPIONCHI polypeptide, or its fragment
CC having 5-HT3 protein function or having an antigenic determinant, or
CC their functional equivalent. This protein was subcloned for mammalian
CC expression. The method of the invention and composition comprising
CC INPIONCHI are useful for the diagnosis, prevention and/or treatment of
CC diseases or conditions associated with T cells, such as inflammatory

CC bowel diseases (including Crohns' disease and ulcerative colitis).
CC multiple sclerosis, psoriasis, rheumatoid arthritis, thrombocytopenia,
CC type 1 diabetes mellitus, asthma, atopic dermatitis, atopic rhinitis,
CC Alzheimer's disease, Parkinson's disease and conjunctivitis, diseases
- CC associated with T cell proliferation such as leukemias, diseases
CC associated with T-cell depletion such as HIV infection, chemotherapy and
CC radiotherapy, and diseases where regulation of T cell activation is
CC required, such as cancers, viral infections, bacterial infections
CC (including tuberculosis) and fungal infections.
XX
SQ Sequence 515 AA;
Query Match 99.8%; Score 2698; DB 9; Length 515;
Best Local Similarity 99.8%; Pred. No. 2.3e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RFDPATHNTVNVNSSGHQCYLPPGIFKSSCYIDVRWPPDVQHCCLKFGSWSYGS 180
DB 121 RFDPATHNTVNVNSSGHQCYLPPGIFKSSCYIDVRWPPDVQHCCLKFGSWSYGS 180
QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVPPTDGGVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVPPTDGGVCGRMACSPTHDEHL 420
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 15
AD52166
ID ADE52166 standard; protein; 502 AA.
XX
AC ADE52166;
XX
XX
DT 12-FEB-2004 (first entry)
XX
DE Human alpha 7 mutant L270T protein SEQ ID NO:4.
XX
XX
KW Q7-6 cell; QM-7 cell; mutant; nicotinic alpha 7 acetylcholine receptor;
KW mutant nicotinic alpha 7 acetylcholine receptor; human.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
PN W02003095976-A2.
XX
PD 20-NOV-2003.
XX

PF 09-MAY-2003; 2003WO-US014553.
XX
PR 09-MAY-2002; 2002US-0378642P.
XX
PA (MEMO-) MEMORY PHARM CORP.
XX
PI Wang D, De Vivo M;
XX
XX WPI; 2004-012192/01.
DR N-PSDB; ADE52165.
XX
PT New Q7-6 cell or QM-7 cell, useful in identifying an agent that modulates
PT the activity or expression of the mutant nicotinic alpha7 acetylcholine
PT receptor.
XX
PS Example 1; SEQ ID NO 4; 48pp; English.
XX
CC The present invention describes a Q7-6 cell or QM-7 cell which comprises
CC a heterologous mutant nicotinic alpha 7 acetylcholine receptor or its
CC protein subunit or a polynucleotide encoding the heterologous mutant
CC nicotinic alpha 7 acetylcholine receptor protein subunit or its fragment
CC or variant. Also described: (1) a method of measuring the activity of the
CC heterologous mutant nicotinic alpha 7 acetylcholine receptor; (2) a
CC method of identifying an agent that activates or inhibits a mutant
CC nicotinic alpha 7 acetylcholine receptor; (3) a method of identifying an
CC agent that modulates the expression of the mutant nicotinic alpha 7
CC acetylcholine receptor; (4) a method of making Q7-6 cell or QM-7 cell;
CC (5) a method of producing a mutant nicotinic alpha 7 acetylcholine
CC receptor protein subunit; and (8) a kit comprising the Q7-6 cell or QM-7
CC cell. The Q7-6 cell or QM-7 cell can be used in identifying an agent that
CC modulates the activity or expression of the mutant nicotinic alpha 7
CC acetylcholine receptor. The present sequence represents the mutant human
CC nicotinic alpha 7 acetylcholine receptor L270T, which is used in an
CC example from the present invention.
XX
SQ Sequence 502 AA;
Query Match 99.6%; Score 2693; DB 8; Length 502;
Best Local Similarity 99.6%; Pred. No. 7.1e-262;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSGGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RFDPATHNTVNVNSSGHQCYLPPGIFKSSCYIDVRWPPDVQHCCLKFGSWSYGS 180
DB 121 RFDPATHNTVNVNSSGHQCYLPPGIFKSSCYIDVRWPPDVQHCCLKFGSWSYGS 180
QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVPPTDGGVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVPPTDGGVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPDLAKILEEVRYIANFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPDLAKILEEVRYIANFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
| | | | | | | | | | | | | | | | | |
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

Search completed: March 28, 2006, 13:29:55
Job time : 190 secs

QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 2
US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; PRIOR FILING DATE: 2004-09-18
; PRIOR FILING DATE: 08/771,737
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2
Query Match 100.0%; Score 2703; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.8e-259;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
DB 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
DB 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 3
US-10-749-075-2
; Sequence 2, Application US/10749075
; Publication No. US20040203033A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/10/749,075
; CURRENT FILING DATE: 2003-12-30
; PRIOR APPLICATION NUMBER: US/08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-10-749-075-2
Query Match 100.0%; Score 2703; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.8e-259;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLALAAASLLHVSLSQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
DB 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCKLKFGSGSYGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKWTTRVILLNWCWFLRMKRPGEDEVKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPGDDLAKILEEVYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDDLAKILEEVYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; Ellis, Steven B.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & Mcauliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 99.8%; Score 2698; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKSEREFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKSEREFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTTMMLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTTMMLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTAVILLNCWFLRMKRPCEDEVKRPACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTAVILLNCWFLRMKRPCEDEVKRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLIYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPASNGNLLIYIGRGLDGVHCVPTDPSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDDLAKILEEVYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGDDLAKILEEVYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-10-740-083-2
; Sequence 2, Application US/10740083
; Publication No. US20040132187A1
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10/740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-2

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGVWLAAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
QY 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKSEREFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKSEREFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240

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QY 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
US-10-769-085-7
; Sequence 7, Application US/10769085
; Publication No. US20050170360A1
; GENERAL INFORMATION:
; APPLICANT: Papke, Roger
; APPLICANT: Placzek, Andon
; TITLE OF INVENTION: Variant Neuronal Nicotinic Alpha-7 Receptor and Methods of Use
; FILE REFERENCE: UF-408
; CURRENT APPLICATION NUMBER: US/10/769,085
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (262)..(281)
; OTHER INFORMATION: TM2 domain
US-10-769-085-7

Query Match          99.8%; Score 2698; DB 5; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.1e-258;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNYNPLERPANDSOPLTIVYFSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNYNPLERPANDSOPLTIVYFSL 60
QY 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RFDATFTNTLVNSSGHCQYLPPIGFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSL 180
Db 121 RFDATFTNTLVNSSGHCQYLPPIGFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
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Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
US-10-434-364-4
; Sequence 4, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-434-364-4

Query Match          99.6%; Score 2693; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 9.7e-258;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNYNPLERPANDSOPLTIVYFSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLYKELVKYNYNPLERPANDSOPLTIVYFSL 60
QY 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGGQIWKPDILLYNSADE 120
QY 121 RFDATFTNTLVNSSGHCQYLPPIGFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSL 180
Db 121 RFDATFTNTLVNSSGHCQYLPPIGFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKSISGIVTLVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
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QY 481 ICTIGILMSAPNFVEAVSKDPA 502
Db 481 ICTIGILMSAPNFVEAVSKDPA 502

RESULT 8
US-10-740-083-10
; Sequence 10, Application US/10740083
; Publication No. US20040132187A1
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Vincent
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-10

Query Match 99.6%; Score 2692; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 1.2e-257;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
Db 1 MRCSGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60

QY 61 QIMDVDEKNQVLTNTINWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTINWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
Db 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTVMRRRPLYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTVMRRRPLYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKCRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKCRPGEDKVRPACQHK 360

QY 361 QRCRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDPA 502
Db 481 ICTIGILMSAPNFVEAVSKDPA 502

RESULT 9
US-10-352-684A-56
; Sequence 56, Application US/10352684A
```

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; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroli, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1NOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-56

Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
Db 1 MRCSGGVWLALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60

QY 61 QIMDVDEKNQVLTNTINWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTINWLQMSWTDHYLQWNSYRGVKTVPDQGIWKPDILLYNSADE 120

QY 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180
Db 121 RPDATFHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFPDPVQHCCKLKFGSWSYGGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTVMRRRPLYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTVMRRRPLYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKCRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKCRPGEDKVRPACQHK 360

QY 361 QRCRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
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Db 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 10
US-10-789-241-8
; Sequence 8, Application US/10789241
; Publication No. US2004018032A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MP103-041PIRNONMIN
; CURRENT APPLICATION NUMBER: US/10789,241
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2003-03-12
; PRIOR FILING DATE: 2003-03-12
; PRIOR FILING DATE: 2003-03-12
; PRIOR FILING DATE: 2003-03-20
; PRIOR FILING DATE: 2003-04-24
; PRIOR FILING DATE: 2003-06-02
; PRIOR FILING DATE: 2003-06-02
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-8

Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKYNPNPLRPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLGLAASLLHVSLLQGEFQKLYKELVKYNPNPLRPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLVNSGGHCQYLPPIGKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Db 121 RFDATFHTNVLVNSGGHCQYLPPIGKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360

Db 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 11
US-10-723-940-124
; Sequence 124, Application US/10723940
; Publication No. US20040185468A1
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freeman, Robert
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor
; TITLE OF INVENTION: Gene
; FILE REFERENCE: VARD-07989
; CURRENT APPLICATION NUMBER: US/10723,940
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 08/956,518
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-940-124

Query Match 99.5%; Score 2690; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.9e-257;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKYNPNPLRPVANDSQPLTVYFSLSL 60
Db 1 MRCSPGGVWLGLAASLLHVSLLQGEFQKLYKELVKYNPNPLRPVANDSQPLTVYFSLSL 60
Qy 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLVNSGGHCQYLPPIGKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Db 121 RFDATFHTNVLVNSGGHCQYLPPIGKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIQLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVGPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGOPPEGDDPLAKILLEEVRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 12

US-10-756-149-5435

; Sequence 5435, Application US/10756149

; Publication No. US20050181375A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND

; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/756,149

; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5435

; LENGTH: 502

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-756-149-5435

Query Match 99.5%; Score 2690; DB 5; Length 502;

Best Local Similarity 99.4%; Pred. No. 1.9e-257;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKYNPLERPVANDSPLTVYFSL 60

Db 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKYNPLERPVANDSPLTVYFSL 60

Qy 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDGOIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDGOIWKPDILLYNSADE 120

Qy 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180

Db 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240

Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240

Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEVKVRPACQHK 360

Db 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEVKVRPACQHK 360

Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420

Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420

Qy 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPAAACVVDRLCLMAFSVFTI 480

Db 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPAAACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502

Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 13

US-10-740-083-12

; Sequence 12, Application US/10740083

; Publication No. US20040132187A1

; GENERAL INFORMATION:

; APPLICANT: Groppi, Vincent

; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; TITLE OF INVENTION: Conductance
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/10/740,083
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: US/09/579,250
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-12

Query Match 99.4%; Score 2688; DB 4; Length 502;

Best Local Similarity 99.6%; Pred. No. 3e-257;

Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKYNPLERPVANDSPLTVYFSL 60

Db 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKYNPLERPVANDSPLTVYFSL 60

Qy 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDGOIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDGOIWKPDILLYNSADE 120

Qy 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180

Db 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240

Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240

Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVVTIVLQYHHDDPGGKMPKWTTRVILLNWCWFLMRKRPGEVKVRPACQHK 360

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Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDSGVVCGRMACSPTHDEHL 420

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Qy 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPAAACVVDRLCLMAFSVFTI 480

Db 421 LHGGQPPEGDDPLAKILEEVRYIANFRCDSEAVCSEWKPAAACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502

Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 14

US-10-740-083-14

; Sequence 14, Application US/10740083

; Publication No. US20040132187A1

; GENERAL INFORMATION:

; APPLICANT: Groppi, Vincent

; APPLICANT: Wolfe, Mark L.

; APPLICANT: Berkenpas, Mitchell B

; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel

; TITLE OF INVENTION: Conductance

; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists

; CURRENT APPLICATION NUMBER: US/10/740,083

; CURRENT FILING DATE: 2003-12-18

; PRIOR APPLICATION NUMBER: US/09/579,250

; PRIOR FILING DATE: 2000-05-25


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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-740-083-14

Query Match          99.2%; Score 2682; DB 4; Length 502;
Best Local Similarity 99.4%; Pred. No. 1.2e-256;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALAAASHLVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLAALAAASHLVSLQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTIVILQYHHDDPGGKMPKWTTRVILLNCWFLMRKRGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVILQYHHDDPGGKMPKWTTRVILLNCWFLMRKRGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVDRCLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVDRCLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 15
US-10-769-085-11
; Sequence 11, Application US/10769085
; Publication No. US20050170360A1
; GENERAL INFORMATION:
; APPLICANT: Papke, Roger
; TITLE OF INVENTION: Variant Neuronal Nicotinic Alpha-7 Receptor and Methods of Use
; FILE REFERENCE: UF-408
; CURRENT APPLICATION NUMBER: US/10/769,085
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Macaca mulatta
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (262)..(281)
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; OTHER INFORMATION:
US-10-769-085-11

Query Match          99.0%; Score 2675; DB 5; Length 502;
Best Local Similarity 98.8%; Pred. No. 5.9e-256;
Matches 496; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIFKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVVTIVILQYHHDDPGGKMPKWTTRVILLNCWFLMRKRGEDKVRPACQHK 360
Db 301 MIIVGLSVVVTIVILQYHHDDPGGKMPKWTTRVILLNCWFLMRKRGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVDRCLCLMAFSVFTI 480
Db 421 LHGGQPPEGDDPLAKILEEVRYIANRFRQDSEAVCSEWKFAACVDRCLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

Search completed: March 28, 2006, 13:38:29
Job time : 169 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:35:49 ; Search time 25 Seconds
(without alignments)
592.247 Million cell updates/sec

Title: US-10-749-075-2

Perfect score: 2703

Sequence: 1 MRCSPGGWTLAASLLHVS.....TIGILMSAPNFVAVSKDPA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	99.8	502	7 US-11-122-144-12	Sequence 12, Appl
2	945	35.0	529	7 US-11-122-144-2	Sequence 2, Appl
3	916	33.9	627	7 US-11-037-829A-1	Sequence 1, Appl
4	887	32.8	627	7 US-11-122-144-6	Sequence 6, Appl
5	884	32.7	498	7 US-11-037-829A-3	Sequence 3, Appl
6	884	32.7	498	7 US-11-122-144-18	Sequence 18, Appl
7	882	32.6	504	7 US-11-122-144-4	Sequence 4, Appl
8	867.5	32.1	494	7 US-11-122-144-10	Sequence 10, Appl
9	861	31.9	502	7 US-11-122-144-14	Sequence 14, Appl
10	850.5	31.5	485	7 US-11-037-829A-11	Sequence 11, Appl
11	849	31.4	502	7 US-11-037-829A-2	Sequence 2, Appl
12	832.5	30.8	491	7 US-11-037-829A-9	Sequence 9, Appl
13	811.5	30.0	495	7 US-11-037-829A-7	Sequence 7, Appl
14	772	28.6	458	7 US-11-122-144-16	Sequence 16, Appl
15	770.5	28.5	468	7 US-11-122-144-8	Sequence 8, Appl
16	571.5	21.1	478	7 US-11-037-829A-4	Sequence 4, Appl
17	555.5	20.6	483	7 US-11-037-829A-5	Sequence 5, Appl
18	232	8.6	485	6 US-10-204-029-7	Sequence 7, Appl
19	221.5	8.2	475	7 US-11-241-631-16	Sequence 16, Appl
20	221.5	8.2	487	7 US-11-241-631-14	Sequence 14, Appl
21	216	8.0	506	7 US-11-241-631-15	Sequence 15, Appl
22	203	7.5	473	7 US-11-169-041-229	Sequence 229, App
23	195	7.2	497	7 US-11-037-829A-15	Sequence 15, Appl
24	193	7.1	474	7 US-11-037-829A-13	Sequence 13, Appl
25	187.5	6.9	422	6 US-10-204-029-4	Sequence 4, Appl

26	187.5	6.9	426	6 US-10-204-029-2	Sequence 2, Appl
27	187	6.9	487	7 US-11-241-631-13	Sequence 13, Appl
28	184.5	6.8	465	7 US-11-037-829A-14	Sequence 14, Appl
29	179.5	6.6	481	6 US-10-512-376-5	Sequence 5, Appl
30	177	6.5	467	6 US-10-512-376-3	Sequence 3, Appl
31	177	6.5	496	6 US-10-512-376-2	Sequence 2, Appl
32	171.5	6.3	345	7 US-11-188-353-10	Sequence 10, Appl
33	171.5	6.3	392	7 US-11-188-353-4	Sequence 4, Appl
34	171.5	6.3	420	7 US-11-188-353-8	Sequence 8, Appl
35	171.5	6.3	459	6 US-10-512-376-6	Sequence 6, Appl
36	171.5	6.3	467	7 US-11-188-353-2	Sequence 2, Appl
37	162	6.0	448	7 US-11-241-631-17	Sequence 17, Appl
38	158	5.8	492	7 US-11-037-829A-12	Sequence 12, Appl
39	112	4.1	226	6 US-10-512-376-8	Sequence 8, Appl
40	110	4.1	504	7 US-11-087-099-1027	Sequence 1027, Ap
41	110	4.1	518	7 US-11-087-099-6795	Sequence 6795, Ap
42	97.5	3.6	556	6 US-10-613-744-8	Sequence 8, Appl
43	96.5	3.6	266	6 US-10-884-730-334	Sequence 334, App
44	96.5	3.6	266	7 US-11-000-463-381	Sequence 381, App
45	94.5	3.5	266	6 US-10-884-730-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-11-122-144-12
; Sequence 12, Application US/11122144
; Publication No. US20050287663A1

GENERAL INFORMATION:

APPLICANT: Gillespie, Alison
Claeys, Brian O.
Chavez-Noriega, Laura Elena
Siegel, Robert
Elliot, Kathryn J.

TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/122,144

FILING DATE: 04-May-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/703,951

FILING DATE: 01-Nov-2000

APPLICATION NUMBER: US 08/487,596

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: WO US94/02447

FILING DATE: 08-MAR-1994

APPLICATION NUMBER: US 08/149,503

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-1993

APPLICATION NUMBER: US 07/938,154

FILING DATE: 30-NOV-1992

APPLICATION NUMBER: US 07/504,455

FILING DATE: 03-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Kohli, Vineet

Db 390 CHFLRLKLSFSYHLSNSVDAREVVEEDRWACAGHVPASVGTLCSHGH-----LHSG 445
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QY 473 MAFSVFTIICIGILMSARNFV 494
Db 506 WLFIVCFGLTIGLFL--PPFL 525

RESULT 3
US-11-037-829A-1
; Sequence 1, Application US/11037829A
; Publication No. US2005025551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Bencherif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-037-829A-1

Query Match 33.9%; Score 916; DB 7; Length 627;
Best Local Similarity 33.9%; Pred. No. 1.7e-76;
Matches 207; Conservative 88; Mismatches 177; Indels 138; Gaps 11;

QY 10 LALAASLL-----HVSLLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
Db 17 LLGTGLLRASSHVEFRAEERLLKKLPSGYNKWRPVANISDVVRFGLSIALIDV 76
QY 66 DEKQVLTNIIWLOMGTWTHYLOMNVSEYGVKTVRPPGQIKWPDILLYNSADERFDT 125
Db 77 DEKNQMTTNVWVKQEMHDKLRWDPADYENVTISRIPSELIWRPDIVLYNNADGFAVT 136
QY 126 FHTNVLVNSGHCQYLPPIGFKSSCYDVRWFFPDVQHCKLKEGWSYGGWSLDL--QMQ 183
Db 137 HLTAKHLFHDGRVQWTPPAIYKSSCIDVTFFPDQDQCTMKFGSWTYDKAKIDLYNMHS 196
QY 184 EADISGVIPIGNGEVDLIGIPKRSERFECCCKEYPPDVTFTVTRRRRTLYVGLMLIIPCVL 243
Db 197 RVQDLDFWESGEWIVDAVGTYNTRYKCECAEYIPDITAFVIRRLPLFTINLIIPCLL 256
QY 244 ISALALLVFLPADSGEKISLGTIVLLSLTFMLVAEIMPATSDVPLIAQYFASMTII 303
Db 257 ISCLTVLVFVLPSECKETLICISVLLSLTVFLLLITELIIPSTVLPIGELYLLFTMIF 316
QY 304 VGLSVVTVTVLYQHHHDPDGGQMPKWTVRVILLNWCANFLMKRPGEDKVRPACQHKQR 363
Db 317 VTLISVITVFLVNLVHRSRPTMTPTWVRVFLDIVPRLLMKRP--SVVKDNC-----R 369
QY 364 CSLASVEMSAVAP-----PPASNG----- 382
Db 370 RLIESMHWKMASRFRWPEPEGEPPATSGTQSLHPPSPFCVPLDVPAEPGPKSPSDQL 429
QY 383 -----NLLYIGFRG--LDG----- 394
Db 430 PPQPLEAEKASPHSPGCPRPSHGTAQPLAKARSLSVQHMSPPGEAVEGGVRCRSRSI 489
QY 395 VHCVPPTDS-----GVVCGRMACSPTHDEHLHGGQP-----PEG----- 429

Db 490 QYCVPRDDAPADQAGALASRNTHSAELPPQPSCKCTCKEPPSSVSPSATVKTR 549
QY 430 -----DPDLAKILEVRYIANFRCODESEAVSEWKPACVDRRLCLMAFSVP 478
Db 550 STKAPPPHPLSPALTRAVEGVQVIADHLKABDTOPSVKEDWKYVAMVIDRIFLWMPFIIV 609
QY 479 TIICTIGILM 488
Db 610 CLIGTVGLEFL 619

RESULT 4
US-11-122-144-6
; Sequence 6, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR. CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/122,144
; FILING DATE: 04-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/703,951
; FILING DATE: 01-Nov-2000
; APPLICATION NUMBER: US 08/487,596
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-122-144-6

Query Match		32.8%; Score 887; DB 7; Length 627;
Best Local Similarity		33.4%; Pred. No. 8.2e-74;
Matches		204; Conservative 87; Mismatches 181; Indels 138; Gaps 11;
QY	10	LALASLL-----HVSIGCFORLYKELVKNYPLRPVANDSQPTVYFSLSLQIMDV 65
DB	17	LLGTGLLRASSHIVETRAHAERLLKLFSGYNKSRPVANISDVVLVRFGLSIAOLIDV 76
QY	66	DEKNQVLTNNIWLQMSWTHYLQWNVSEYGVKTVRPPDQIWKPDILLVNSADERFDAT 125
DB	77	DEKNQMTTNNVWQKWBHDKLWDPADYENVTISIRPSELVWRPDIALYNNADGDAAT 136
QY	126	FHTNVLVNSGHCQYLPPIGFKSSCYIDVRPFQVQHCKLFGSGWSYGGWSLDL--OMQ 183
DB	137	HLTKAHLFDHGRVORTPEAIYKSSCSIDVTFPPDQNCNCTMKFGSWTYDKAKIDLVMHS 196
QY	184	EADISYIYNGEWDLVGIFGKRSERYECKEYPDVTVTVMRRRTLYYGLNLLIPCVL 243
DB	197	RVDQLDFWESGEWLIJSDAVGTVNTRKYECCEAIYDITYAYAIRLPLFTYTNLIIPWLL 256
QY	244	ISALALLVLLPADSGEKISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAOYFASTMLI 303
DB	257	ISCLTALVYLFSECGEKITLCSVLSTVFLLLITEIIPSTSLVPLIGELVLLFTMIF 316
QY	304	VGLSVVTVVIVLYQHHDDGGKMPKWTTRVILLNMCWFLRMKRPGEDKVRPACQHKQRR 363
DB	317	VTLISAIITVFLNVHRSRPTHMTPTVVRVFLDIIVPRLLMKRP--SVVKDNC-----R 369
QY	364	CSLASVEMSAVAP-----PPASNG----- 382
DB	370	RLTESMHKMASAPRFWPEPEGBPPATSGTQSLHPPSPFCVPLDVPAEPGCKSPSDQL 429
QY	383	-----NLLYIGFRG--LDG----- 394
DB	430	PPQPLEAKSPHSPGRCRPHGTQAPGLAKARSLSVQHMSSPGEAVEGGVRCRSRI 489
QY	395	VHCVPPTPDS-----GYVCGRMACSPHDEHLLHGQP-----PEG----- 429
DB	490	QYCVPRDDAAPADGQAAGALASRNSHSAELPPDPQSPCKCTCKEPPSSVPSATVKTR 549
QY	430	-----DPDLAKILIEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVF 478
DB	550	STKAPPPLPLSPALSRVGEVQYIADHLKABEDTDFSVKEDWKYAMVIDRFLWFIIV 609
QY	479	TIICITGILM 488
DB	610	CLUGVGLFL 619
RESULT 5		
US-11-037-829A-3		
; Sequence 3, Application US/11037829A		
; Publication No. US20050255551A1		
; GENERAL INFORMATION:		
; APPLICANT: Targacept, Inc		
; APPLICANT: Catholic Healthcare West		
; APPLICANT: Bencherif, Merouane		
; APPLICANT: Lukae, Ronald J.		
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric		
; FILE OF INVENTION: Nicotinic Receptor Subunits		
; FILE REFERENCE: T103 1520.PCT		
; CURRENT APPLICATION NUMBER: US/11/037,829A		
; CURRENT FILING DATE: 2005-01-18		
; PRIOR APPLICATION NUMBER: US 60/397,380		
; PRIOR FILING DATE: 2002-07-19		
; NUMBER OF SEQ ID NOS: 15		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 3		
; LENGTH: 498		
; TYPE: PRT		
; ORGANISM: Homo sapien		
US-11-037-829A-3		
Query Match		32.7%; Score 884; DB 7; Length 498;
Best Local Similarity		39.0%; Pred. No. 1.1e-73;
Matches		184; Conservative 94; Mismatches 166; Indels 28; Gaps 9;
QY	26	QRKLYKELVK--NYNPLRPVANDSQPTVYFSLSLQIMDVDEKNQVLTNNIWLQMSWT 83
DB	27	BEKLMDLLNTRVNNLRIPATSSQLISIKLQLSLAQLISVNEREQIMTTNNVLKQEW 86
QY	84	DHYLQWNVSEYGVKTVRPPDQIWKPDILLVNSADERFDATFHTNVLVNSGHCQYLP 143
DB	87	DYRLTWNSRYEGVNLIRIPAKRIWLPDILVLYNNADGTIEVSVTNLIIVRSNGSVLW 146
QY	144	GIFKSSCYIDVRPFQVQHCKLFGSGWSYGGWSLD--LQMOEADISGYIPNGEWDLV 201
DB	147	AIYKSACKIEVKYFFPDQNCNCTLKFRSTYDHTEDMWLMTPTASMDDFTPSGEWDI 206
QY	202	PKRSERYECKEKP-YPDVTVTVMRRRTLYYGLNLLIPCVLISALALLVLLPADSGE 260
DB	207	PGRRTVN----PQDPSYVDVYDFIIRKPLFTYTNLIIPCVLTTLLAILFYLPSDCGE 262
QY	261	KISLGTIVLLSLTTFMLLVAEIMPATSDSVPLIAOYFASTMLIIVGLSVVTVVIVLYQHH 320
DB	263	KMTLCISVLLAUTFPILLISKIVPPTSLDVPLIGLYLMTFTWLVFTSVTSVCVNLVHR 322
QY	321	DPDGGKMPKWTTRVILLNMCWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVAPPAS 380
DB	323	SPSTHTMAPWVKRCFLKLPFLFMKRPGPS-SPARAFPPSKSCVTKPEATATSTSPSN 381
QY	381	NGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPT---HDEHLLHGQPPGEGDPLAKI 436
DB	382	FYGNSMYF-----VNPASAAKSPAGSTPVAIPRDFWFLRSSGRFRQ---DVQEA 427
QY	437	LEEVEYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVFTIICITGILM 488
DB	428	LEGVSFIAQHMKNDDQSVVEDMKYVAMVVDRLFLWFMFVFCVLGTGVLFL 479
RESULT 6		
US-11-122-144-18		
; Sequence 18, Application US/11122144		
; Publication No. US20050287663A1		
; GENERAL INFORMATION:		
; APPLICANT: Gillespie, Alison		
; Claeps, Brian O.		
; Chavez-Noriega, Laura Elena		
; Siegel, Robert		
; Elliott, Kathryn J.		
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS		
; OF NEURONAL NICOTINIC ACETYLCHOLINE		
; RECEPTOR, CELLS TRANSFORMED THEREWITH,		
; AND RECOMBINANT CELL LINE EXPRESSING		
; NUMBER OF SEQUENCES: 18		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Merck & Co., Inc.		
; STREET: 126 E. Lincoln Avenue		
; CITY: Rahway		
; STATE: NJ		
; COUNTRY: USA		
; ZIP: 07065-0907		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: PatentIn Release #1.0, Version #1.25		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/11/122,144		
; FILING DATE: 04-May-2005		
; CLASSIFICATION: <Unknown>		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US/09/703,951		
; FILING DATE: 01-Nov-2000		
; APPLICATION NUMBER: US 08/487,596		

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/
/
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: WO US94/02447
/ FILING DATE: 08-MAR-1994
/ APPLICATION NUMBER: US 08/149,503
/ FILING DATE: 08-NOV-1993
/ APPLICATION NUMBER: US 08/028,031
/ FILING DATE: 08-MAR-1993
/ APPLICATION NUMBER: US 07/938,154
/ FILING DATE: 30-NOV-1992
/ APPLICATION NUMBER: US 07/504,455
/ FILING DATE: 03-APR-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kohli, Vineet
/ REGISTRATION NUMBER: 37,003
/ REFERENCE/DOCKET NUMBER: SD99511A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-3889
/ TELEFAX: 732-594-4720
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 498 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-11-122-144-18

Query Match      32.7%; Score 884; DB 7; Length 498;
Best Local Similarity 39.0%; Pred. No. 1.1e-73;
Matches 184; Conservative 94; Mismatches 166; Indels 28; Gaps 9;

QY 26 QRLKLYELVK--NYNLEPVPANDSOPLTIVYSLSLQIMDVDEKNQVLTNNIQLMSWT 83
DB 27 ESKMDDLKTRNNLIRPATSSSSLSIKQLSLAQLISNREQIMTTNNVLKQWT 86
QY 84 DHYLQWNVSEYGVKTVRPPDGOIWKPDILLVNSADERFDATFHTNVLVNSGHCQYLPP 143
DB 87 DRLTWNSRYEGVNLIRIPAKRIMLPDIVLYNADGTVEVSYYTNLIVRSNGSVLWLP 146
QY 144 GIFKSCYIDVRWPPDVQCHLKFSGWSYGGWSLD--LQMEADIISGYIPNGEWDLVGI 201
DB 147 AIYKSAKIEVKYFPDQCNCTLKFRSTYDHTIDVLMWLTPTASMDPTPSGEWDVAL 206
QY 202 PKRSEFYECCKEP-YPDVTFTVWRRRTLYGLNLLIPCVLISNALALLVLLPADSGE 260
DB 207 PGRVTN-----PDQPSYVDVTDYFIKPKPLFTYINLIIPCVLTLLAILVFLPSDCGE 262
QY 261 KISLGIITVLLSTFMLLVAETMPATSDSVPLIAQVFASTMIIVGLSVVVTIVLQYHH 320
DB 263 KMTLCISVLLATFFLLLSKIVPTSLDVPLIGKYLMTNVLVTFISIVTSCVLNVHR 322
QY 321 DPDGGKMPKWTIRVILLNWCWFLMKRPGEDKVRPACQHKQRCSLASVEMSAVPPAS 380
DB 323 SPSTHTMAPWVKRCFLHLKPTLEFMKRPGPS-SPARAPPKSKCVTKPEATATSTSPN 381
QY 381 -NGNLYIGRGLDGVCHVPTDSDGVVCGMACSPT---HDEHLHGGOPPGSDPLAXI 436
DB 382 FTGNSMYF-----VNPASASKSPAGSTPVAIPRDFWLKSSGRFRQ---DVQEA 427
QY 437 LEEVRYIANRFRQDSEAVCSSEKFAACVDRCLCMAFSVFTICTIGILM 488
DB 428 LSGVSFIAQMKNDDEDSQSVEDWKYVAMVDRFLFWVFMFVCLVGLTGLFL 479

RESULT 7
US-11-122-144-4
; Sequence 4, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
```

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/
/
/ Elliott, Kathryn J.
/ TITLE OF INVENTION: DNA ENCODING HUMAN ( AND ( SUBUNITS
/ OF NEURONAL NICOTINIC ACETYLCHOLINE
/ RECEPTOR, CELLS TRANSFORMED THEREWITH,
/ AND RECOMBINANT CELL LINE EXPRESSING
/
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: 126 E. Lincoln Avenue
/ CITY: Rahway
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07065-0907
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/122,144
/ FILING DATE: 04-May-2005
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/703,951
/ FILING DATE: 01-Nov-2000
/ APPLICATION NUMBER: US 08/487,596
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: WO US94/02447
/ FILING DATE: 08-MAR-1994
/ APPLICATION NUMBER: US 08/149,503
/ FILING DATE: 08-NOV-1993
/ APPLICATION NUMBER: US 08/028,031
/ FILING DATE: 08-MAR-1993
/ APPLICATION NUMBER: US 07/938,154
/ FILING DATE: 30-NOV-1992
/ APPLICATION NUMBER: US 07/504,455
/ FILING DATE: 03-APR-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kohli, Vineet
/ REGISTRATION NUMBER: 37,003
/ REFERENCE/DOCKET NUMBER: SD99511A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-3889
/ TELEFAX: 732-594-4720
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 504 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-122-144-4

Query Match      32.6%; Score 882; DB 7; Length 504;
Best Local Similarity 35.7%; Pred. No. 1.8e-73;
Matches 179; Conservative 98; Mismatches 170; Indels 54; Gaps 7;

QY 10 LALAASLHLVSLQGSFORLKYKELVKNYNIPLERPANDSQPLTVYFSLSLQIMDVDEKN 69
DB 18 LLLLLLPLVARASAEHRLPERLPEDYNEIIRPVANVSDPVIHFVYSMSQLVKYDEVN 77
QY 70 QVLTTNIMQLQSWTDHYLQWNVSEYGVKTVRPPDGOIWKPDILLVNSADERFDATFHTN 129
DB 78 QIMETNLWLKQIWNQYDKLKNWPSDYGGAEFMKRVPAQKIWKPDIVLYNNAVGDFQVDDKTK 137
QY 130 VLVNSSGHQCVLPGLPKSSCYIDVRWPPDVQCHLKFSGWSYGGWSLDLQW--QEADI 187
DB 138 ALLKKTGVETWIPPAIFKSSCKIDVTYFPDQNTMKFGSWSYKAKIDLVLISSMNL 197
QY 188 SGYIPNGEWDLVGIPGKSERPFYECCKBPYPDVTFTVWRRRTLYGLNLLIPCVLISAL 247
DB 198 KDYWESGEWAIKAPGYKHDIKYSCCEIYDITYSLXIRRLSLFVTIXLIIRWLIISPI 257
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QY 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASMTIIVGLS 307
Db 258 TVVSYLPSDCGKVTLCISVLLSVFLVITETIPSTSLVPLIGEYLLXTMICVTLS 317
QY 308 VVVTVILVQYHHDDPGGKMPKWTWVILLNCAWFLMKRPGEDKVRPACQHKQRCSLA 367
Db 318 IDITVCVLNVHRTPTHTTPSWVKTVFLXLLPRVNMXMRP-----T 359
QY 368 SYVMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDS-----GVCGRMACSPTHDEHL-- 420
Db 360 SNEGNAQKPRPLYGAE-----LSNLNCFPSAESKCKEGYPCODGMCYCHHRIKI 411
QY 421 -----LHGQPPG-----DPLAKILEVRYIANFRQDSSEAVCSWKPAA 464
Db 412 SNFSANLTRSSSESVDVLSLSALSPETKEAQSVKYIAENKQAQNEAKETQDDWKVA 471
QY 465 CVVDRLCMAFSVFTIICIG 485
Db 472 MVIDRIFLW---VFTLVCLIG 489

RESULT 8

US-11-122-144-10
; Sequence 10, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR, CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/122,144
; FILING DATE: 04-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/703,951
; FILING DATE: 01-Nov-2000
; APPLICATION NUMBER: US 08/487,596
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: SD99511A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3889

; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-11-122-144-10

Query Match 32.1%; Score 867.5; DB 7; Length 494;
Best Local Similarity 35.9%; Pred. No. 3.8e-72;
Matches 178; Conservative 100; Mismatches 173; Indels 45; Gaps 8;

QY 6 GG--VWLALAAALLHVSILQGEFQRKLYKELVKNYNPLRPVANDSQPLTVVFSLSLQIM 63
Db 12 GGLCLNLCVTFPPFGKCGVCATEERLFHKLFSHYNQFIRPVENVSDPTVHFEVAITQLA 71
QY 64 DVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLVNSADERPD 123
Db 72 NVDEVNQIMETNLWLRIHWNDYKLRWDPMEDYGTETLRVPADKIWKPDIVLYNNAVGDFQ 131
QY 124 ATFTNVLNVSCHCOYLPRIKSSCYIDVRWEPDVOHCKLKEGWSYCGWSLDLQW- 182
Db 132 VEGTKALLKYNQMTWTPPAIFKSSCPMDITFFPFHQNCSLKFGSWTYDKAEIDLII 191
QY 183 -QEADISGYIPNGEWDLVGIPGKESERFEYCKBPYPDVTFTVMRRRTLYGLMLLIPC 241
Db 192 GSKVMDNDFWENSEWEIIDASGYKHDIKYNCCEIYTDITYFYIRRLPMFTINLIIPC 251
QY 242 VLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASMT 301
Db 252 LFISFLTVLVPFLPSDCGKVTLCISVLLSLTVFLVITETIPSTSLVPLVGEYLLFTM 311
QY 302 IIVGLSVVVTVILVQYHHDDPGGKMPKWTWVILLNCAWFLMKRP-----GEDKVR 354
Db 312 IFVTLSIVTVFVLNIHYRTPTHTTPRWKVTFLKLLPQVLLMRWPLDKTRGTGSDAVP 371
QY 355 PACQHKQRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTPDSDGVVCGRMACSP 414
Db 372 RGLARRPAKGL-----ASHGEPRHL-----KECFCHKSNELATSKRLSHQ 415
QY 415 -----THDEHLHGGQPPGDPDLAKILEVRYIANFRQDSSEAVCSWKPAA 469
Db 416 LQWVENSEH-----SPEVEDVINSQVIAENKMSHNETKEVEDDKVYAMVVDR 465
QY 470 LCLMAFSVFTIICIG 485
Db 466 VFLW---VFTLVCLIG 478

RESULT 9

US-11-122-144-14
; Sequence 14, Application US/11122144
; Publication No. US20050287663A1
; GENERAL INFORMATION:
; APPLICANT: Gillespie, Alison
; Claeps, Brian O.
; Chavez-Noriega, Laura Elena
; Siegel, Robert
; Elliott, Kathryn J.
; TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
; OF NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR, CELLS TRANSFORMED THEREWITH,
; AND RECOMBINANT CELL LINE EXPRESSING
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907

COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: PatentIn Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/11/122,144	
FILING DATE: 04-May-2005	
CLASSIFICATION: <Unknown>	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US/09/703,951	
FILING DATE: 01-Nov-2000	
APPLICATION NUMBER: US 08/487,596	
FILING DATE: 07-JUN-1995	
APPLICATION NUMBER: WO US94/02447	
FILING DATE: 08-MAR-1994	
APPLICATION NUMBER: US 08/149,503	
FILING DATE: 08-NOV-1993	
APPLICATION NUMBER: US 08/028,031	
FILING DATE: 08-MAR-1993	
APPLICATION NUMBER: US 07/938,154	
FILING DATE: 30-NOV-1992	
APPLICATION NUMBER: US 07/504,455	
FILING DATE: 03-APR-1990	
ATTORNEY/AGENT INFORMATION:	
NAME: Kohli, Vineet	
REGISTRATION NUMBER: 37,003	
REFERENCE/DOCKET NUMBER: SD99511A	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 732-594-3889	
TELEFAX: 732-594-4720	
INFORMATION FOR SEQ ID NO: 14:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 502 amino acids	
TYPE: amino acid	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
US-11-122-144-14	
Query Match	31.9%; Score 861; DB 7; Length 502;
Best Local Similarity	35.0%; Pred. No. 1.5e-71;
Matches 180; Conservative 102; Mismatches 192; Indels 40; Gaps 9;	
QY	2 RCGPGVWLAALASLLHVSLOG--EFORKYKELV--KNYNPLERPVANDSOPLTVYFSL 58
DB	4 RCGFVALLGFLRLCSGWGTDEERLVEHLDPKYNKLRIPATNGSELVTVOLMVS 63
QY	59 LQIQMDVDEKQVLTNNIQLQMSWTDHYLQWNSYGPVKTVPDPGQIKWPDILLNYS 118
DB	64 LAQLISVHERQIMTTNVLMTQEWEDYRLTWKPEFDNMCKVRLPSKHILPDVVLNNA 123
QY	119 DERPDATFTNVLNSSGHCQVLPQGIKSSCCIDVRWPPFDVQCKLKFGSWYGSWL 178
DB	124 DGMYSFYSNAVSVYDGSIFMLPPAIYKSAKIEVGFPPDQCNCKMFKPSWTYDTEI 183
QY	179 DLQMQE--ADISGYINGEWDLVGIPGRKSEFYECCKEPEYDVTFTVMRRRTLYYGLN 236
DB	184 DLVLSKESVSLDFTSGEMDVALPGRNPPD---STVVDIYDFIIRKELFTIIN 240
QY	237 LLIPCVLISALALLVFLPADSGEKISLGITVLLSLTTFMLVAEIMPATSDSVPLIAQY 296
DB	241 LIIPCVLITSLALVFLPSDCGERKMTLCISVLLALTTFLLLSKIVPPTSLDVPVGVKY 300
QY	297 FASTMIIVGLSVVTVIVLYHHDDPGKMPKTRVILLNWCANFLBMRKPGEDKVRPA 356
DB	301 LMFTWLVTFSTVTSVCLNVHRSPTTHMAPVKVVFLEKLPALLFMQPFRRHCARQ 360
QY	357 CQHKQRCSLASVEMSAVAPPASNGNLAY1-----GFRGLDGVHCVPTPD---SGVVC 407
DB	361 LRURRQRREGAGALFFREAPGADSCCTCFNVRASVQGLAGAFGAPVAPGQRSGEPC 420
QY	408 GRMACSPTHDEHLLHGQPGEPDOLAKILEEVRYIANFRFCODESEAVCSSEWKFACV 467

CURRENT APPLICATION NUMBER: US/11/037,829A
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/397,380
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 495
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human nACHR alpha4-mouse 5HT3-FLAG chimera
US-11-037-829A-7

Query Match 30.0%; Score 811.5; DB 7; Length 495;
Best Local Similarity 36.1%; Pred. No. 5.7e-67;
Matches 180; Conservative 78; Mismatches 169; Indels 71; Gaps 9;
QY 10 LALAASLL----HVSLLQSGFQRLKYLKLVNPNPLRPVANDSQPLTVYFSLSLQIMDV 65
DB 17 LLTGTLGRASSHVEFRAHBERLLKLPFGYNKWRPVANISDVVLRFGLSIAQLIDV 76
QY 66 DEKNQVLTNNIWLQMSWTHYLOMNVSEYGVKTVRFPDQIWKPDILLYNSADERFDAT 125
DB 77 DEKNQMTTNNVYKQSHDYKLRWDPADYENVTSIRIPSELIWRPDIVLYNNADGFAVT 136
QY 126 FHTNVLVNSGHCQYLPFGIPKSSCYIDVRPPFDVQHKLKFGSWYSGNSLDL--QM 183
DB 137 HLTKAHLFDHGRVQMTPPAIYKSSCSIDVTFFPDQOQCTMKRFGSWYDKAKIDL 196
QY 184 EADISYVINGEWDLVGIPKRSERYECKBPDPVTVTMMRTLYGLNLLIPCVL 243
DB 197 RVDQDFWESGEVIVDAGVTNRYKCAEYIPDITAFIRRLPFTYINLIIPCLL 256
QY 244 ISALALLVFLPADSGEKISLGITVLLSTLTFMLLVAEIMPATSDSVPLIAQYFASTMI 303
DB 257 ISCLTVLVFLPSECEKILCLISVLLSTVFLLLTEIIPSTLVIPLIGYVFCVMA 316
QY 304 VGLSVVTVIVLYQHHDDPGGKMPKQWTRVILLNWCAMFLMKRPOEDKVRPACQHK 363
DB 317 LVISLAETIFIVRLVHKQDLQRPVDPWLRHLVDRIAWILCL---GEQPM----- 363
QY 364 CSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLL 423
DB 364 -----AHRPPATFQAN-----KTDD-----CSGSDLLPANGNCHSHV 395
QY 424 G-----QPPEGDPDLA--KILBEVRYIANFRQDSEAVCSWEKFAACV 466
DB 396 GGPQDLEKTPRGSGPLPPPREASLAVRGLQELSSIRHFLEKRDREMRVARDLVRGV 455
QY 467 VDR-----LCUMAFSV 477
DB 456 LDRLLPRIYLLAVLAYSI 473

RESULT 14

US-11-122-144-16
Sequence 16, Application US/11122144
Publication No. US20050287663A1

GENERAL INFORMATION:

APPLICANT: Gillespie, Alison

Claeys, Brian O.

Chavez-Noriega, Laura Elena

Siegel, Robert

Elliot, Kathryn J.

TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSER: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/122,144
FILING DATE: 04-May-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/703,951

FILING DATE: 01-Nov-2000

APPLICATION NUMBER: US 08/487,596

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: WO US94/02447

FILING DATE: 08-MAR-1994

APPLICATION NUMBER: US 08/149,503

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-1993

APPLICATION NUMBER: US 07/938,154

FILING DATE: 30-NOV-1992

APPLICATION NUMBER: US 07/504,455

FILING DATE: 03-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Kohli, Vineet

REGISTRATION NUMBER: 37,003

REFERENCE/DOCKET NUMBER: SD99511A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3889

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 458 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-11-122-144-16

Query Match 28.6%; Score 772; DB 7; Length 458;

Best Local Similarity 33.4%; Pred. No. 2.3e-63;

Matches 162; Conservative 92; Mismatches 151; Indels 80; Gaps 9;

QY 24 EFQRLKYLKLVNPNPLRPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNNIWLQMSWT 83

DB 27 ENEDALLRHLFGYQKQWVRPVLHSDNTIKVYFGLKISQLVDVDEKNQVLTNNIWLQMSWT 86

QY 84 DHYLQWNVSEYGVKTVRFPDQIWKPDILLYNSADERFDATFHTNVLVNSGHCQYLP 143

DB 87 DHKLAWNPDDYGGIHSIKVPSESLMPLDVLFPENADGRFEGSLMTKVIKSNGTVVWTP 146

QY 144 GIFKSSCIDVRWFPDVOHQCKLKFGSWYSGNSLDLQW--QEADISGYIPNGEWDLV-- 199

DB 147 ASYKSSCTMDVTFPDRQNCMKFGSWTYDGTVDLILINENVDRKOPFDNGEWELNA 206

QY 200 -GIPGRSEREFYECCKEYPDVTFVTMMRTLYYGLNLLIPCVLISALALLVFLPADS 258

DB 207 KGMKNRRDGVYS-----YPFITYSFVLRPLFFVTLIIIPCLGUSFTVVLVFLPSDE 261

QY 259 GKISGLITVLISLTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVILVQVH 318

DB 262 GEKLSLSTVLSVLTVFLVIEEIIIPSSSKVLIPLIGEVLLFTMIFTLSIIVTVFVINVH 321

QY 319 HHDPDG-GKMPKQWTRVILLNWCAMFLMK-----RPEGDKVRPACQ-----HKQRCSL 366

DB 322 HRSSSTYHPMAPWVKRLFLQKLPKLLCMKDHVDYSSPEKESQPVVVKVLEKKQKQL 381

QY 367 ASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLLHGGOP 426

Db 382 -----SDGEKLVAF----- 391

QY 427 PEGDPLAKILEVRVYIANFRQDSEAVCEWKEFAACVDRCLCMARFVFTIICIGI 486

Db 392 -----LEKAADSIRYISRHVKKEHPISQVQDMKFEVAQVLDRIFLWLFLI--VSATGSV 443

QY 487 LMSAP 491

Db 444 LIFTP 448

RESULT 15

US-11-122-144-8

; Sequence 8, Application US/11122144

; Publication No. US20050287663A1

; GENERAL INFORMATION:

; APPLICANT: Gillespie, Alison

; Claeps, Brian O.

; Chavez-Noriega, Laura Elena

; Siegel, Robert

; Elliott, Kathryn J.

TITLE OF INVENTION: DNA ENCODING HUMAN (AND (SUBUNITS

OF NEURONAL NICOTINIC ACETYLCHOLINE

RECEPTOR, CELLS TRANSFORMED THEREWITH,

AND RECOMBINANT CELL LINE EXPRESSING

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/11/122,144

APPLICATION NUMBER: US/11/122,144

FILING DATE: 04-May-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/703,951

FILING DATE: 01-Nov-2000

APPLICATION NUMBER: US 08/487,596

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: WO US94/02447

FILING DATE: 08-MAR-1994

APPLICATION NUMBER: US 08/149,503

FILING DATE: 08-NOV-1993

APPLICATION NUMBER: US 08/026,031

FILING DATE: 08-MAR-1993

APPLICATION NUMBER: US 07/938,154

FILING DATE: 30-NOV-1992

APPLICATION NUMBER: US 07/504,455

FILING DATE: 03-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Kohli, Vineet

REGISTRATION NUMBER: 37,003

REFERENCE/DOCKET NUMBER: SD99511A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3889

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 468 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-11-122-144-8

Query Match 28.5%; Score 770.5; DB 7; Length 468;

Best Local Similarity 32.7%; Pred. No. 3.2e-63;

Matches 166; Conservative 93; Mismatches 163; Indels 85; Gaps 10;

QY 2 RCSPGGWMLAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQ 61

Db 23 RCGLAAGAGQAQRLSEPSSTAKHEDSLKDLFQDYERWVRPVEHLNDKIKIKFLAISQ 82

QY 62 INDVDEKNOVLTTNIWLQMSWTDHVLQNVSEYPCVKTVRPDDGOIKWPKDILLNSADER 121

Db 83 LVDVDEKNQMLTTNWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFNDAGR 142

QY 122 FDATHTNVLVNSGCHCOYLPPIGPKSSCYIDVRWFFPDVQHCCLKFGGSWSYGGMSLDLQ 181

Db 143 PEGT-STKTVIRYNGTVTWTTPANYKSSCTIDVTFPFDLQNCMKFSGSWYDGSQVDII 201

QY 182 MOEADIS--GYIPNGEWDLVGIPGRSRERFYECCKEPPYDVFTVTMRRRTLYYGLNLI 239

Db 202 LEDQVDKRDFFDNGEWEIVSATGSKGNRTDSCWYPY--VTYSFVKRLPLFYTLFLII 259

QY 240 PCVLISALALLVFLLPADSGEKISLGIYVILSLTTFMLLVAEIMPATSDSVPLIAQYAS 299

Db 260 PCIGLSFLTIVLVFLPSNEGEKICLCTSVLVSALTIVFLVIBIEIIPSSKVIPLIGEYLVF 319

QY 300 TMIIVGLSVVTVIVLVQVHHDDPDGGKMPKWTVRILLNCAWFLRMKRPGEKVRPACOH 359

Db 320 TMIFVTLSIMVTVPAINIHH-----RSSSTH 345

QY 360 KQRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGSGVGVGRMACSPH--- 416

Db 346 -----NAMAP-----LVKRIF-----LHTLP-----KLLCMRSHVDR 372

QY 417 -----DEHLLHGGOPPEGDPDLAKILEVRYIANRPRCODESEAVCEWKEFAACVDRCL 472

Db 373 YFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKMKENDRVVEVDWKFIQAQVLDRMFL 432

QY 473 MAFSVFTIICITIGILMSAPNFVEAVSK 499

Db 433 WTFLEVSIVGSLGL-----FVPVIYK 453

Search completed: March 28, 2006, 13:39:00

Job time : 26 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2006, 13:30:14 ; Search time 42 Seconds
(without alignments)
1150.019 Million cell updates/sec

Title: US-10-749-075-2
Perfect score: 2703
Sequence: 1 MRCSPGGVWLAALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2690	99.5	502	1 ACHUA7	nicotinic acetylch
2	2690	99.5	502	2 G02259	alpha 7 neuronal n
3	2545	94.2	502	2 A57175	nicotinic acetylch
4	2531	93.6	502	2 T01378	nicotinic receptor
5	2429	89.9	502	2 JN0113	nicotinic acetylch
6	1816.5	67.2	511	2 JH0173	alpha-bungarotoxin
7	1107.5	41.0	498	2 S68588	nicotinic acetylch
8	1089.5	40.3	560	2 T19622	hypothetical prote
9	998	36.9	461	2 T25671	nicotinic acetylch
10	947	35.0	557	2 S12359	hypothetical prote
11	944	34.9	542	2 T19862	hypothetical prote
12	942.5	34.9	511	2 A40110	nicotinic acetylch
13	938.5	34.7	459	2 S14703	nicotinic acetylch
14	937.5	34.7	528	1 ACCH2N	nicotinic acetylch
15	936.5	34.6	503	2 A53956	nicotinic acetylch
16	935.5	34.6	576	1 ACFFA2	nicotinic acetylch
17	934	34.6	622	1 ACCH4N	nicotinic acetylch
18	933	34.5	502	2 A37040	nicotinic acetylch
19	922	34.1	567	1 ACFFA1	nicotinic acetylch
20	916	33.9	627	2 JC4021	nicotinic acetylch
21	915.5	33.9	495	2 S60589	acetylcholine rece
22	913.5	33.8	625	2 A28456	nicotinic acetylch
23	912	33.7	495	2 B35721	nicotinic acetylch
24	898	33.2	494	2 T09289	nicotinic acetylch
25	895	33.1	517	2 A30992	probable nicotinic
26	887.5	32.8	499	2 A24572	nicotinic acetylch
27	884	32.7	498	2 G02421	nicotinic acetylch
28	877	32.4	521	1 ACFFNN	nicotinic acetylch
29	876.5	32.4	491	1 ACCHNN	nicotinic acetylch

30	876	32.4	470	2 A39218	nicotinic acetylch
31	874	32.3	512	2 B37014	nicotinic acetylch
32	861	31.9	502	2 S10505	nicotinic acetylch
33	857	31.7	457	2 S13872	nicotinic acetylch
34	850	31.4	457	2 A24383	nicotinic acetylch
35	849.5	31.4	511	2 T43634	acetylcholine rece
36	848	31.4	445	2 I49458	nicotinic acetylch
37	845	31.3	457	1 ACBOA1	nicotinic acetylch
38	844.5	31.2	500	2 S12899	nicotinic acetylch
39	842	31.2	457	1 ACHUA1	nicotinic acetylch
40	839	31.0	456	1 ACCHAN	nicotinic acetylch
41	838.5	31.0	503	2 JH0174	hypothetical prote
42	837.5	31.0	468	2 T24724	nicotinic acetylch
43	832.5	30.8	479	2 A55382	nicotinic acetylch
44	829.5	30.7	457	2 S08162	nicotinic acetylch
45	828	30.6	474	2 T27006	hypothetical prote

ALIGNMENTS

RESULT 1

ACHUA7
Nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A>Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the Sf
ombrs expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-502 <PEN>
A:Cross-references: UNIPROT:P36544; UNIPARC:UPI000016A581; EMBL:X70297; NID:9496606; PDB:
A:Experimental source: brain neuroblastoma cell line SHSY-5Y
R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heingemann, S.
Genomics 19, 379-381, 1994
A>Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic re
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194
A:Molecule type: mRNA
A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>
A:Cross-references: UNIPARC:UPI000016A6CF; GB:Z23141; NID:9457736; PIDN:CAA80672.1; PID:9
A:Experimental source: retina
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:I38751; OMIM:118511
A:Map position: 15q14-15q14
A>Note: defects in this gene have been associated with mental retardation and schizophrenia
C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains and
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predic
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46.90.133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:150-164/Disulfide bonds: #status predicted
F:365.413/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 99.5%; Score 2690; DB 1; Length 502;
Best Local Similarity 99.4%; Pred. No. 2.6e-219;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MRCSPGGVWLAALAAASLLHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSL 60	
Db	1	MRCSPGGVWLAALAAASLLHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSL 60	
Qy	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADE 120	
Db	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADE 120	
Qy	121	RFDATFHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL 180	
Db	121	RFDATFHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL 180	
Qy	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240	
Db	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240	
Qy	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300	
Db	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300	
Qy	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLMKRPGEDKVRPACQHK 360	
Db	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLMKRPGEDKVRPACQHK 360	
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGPRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420	
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGPRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420	
Qy	421	LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVDRCLCLMAFSVFTI 480	
Db	421	LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVDRCLCLMAFSVFTI 480	
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	
RESULT 2			
G02259			
alpha 7 neuronal nicotinic acetylcholine receptor - human			
C:Species: Homo sapiens (man)			
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004			
C:Accession: G02259			
R:Leonard, S.			
submitted to the EMBL Data Library, November 1995			
A:Reference number: H00936			
A:Accession: G02259			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-502 <LEO>			
A:Cross-references: UNIPROT:P36544; UNIPARC:UPI0000169BDC; EMBL:U40583; NID:g1125076; PI			
C:Superfamily: acetylcholine receptor			
Query Match 99.5%; Score 2690; DB 2; Length 502;			
Best Local Similarity 99.4%; Pred. No. 2.6e-219;			
Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MRCSPGGVWLAALAAASLLHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSL 60	
Db	1	MRCSPGGVWLAALAAASLLHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSL 60	
Qy	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADE 120	
Db	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADE 120	
Qy	121	RFDATFHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL 180	
Db	121	RFDATFHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDL 180	
Qy	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240	
Db	181	QMOEADISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240	

Qy	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300	
Db	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300	
Qy	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLMKRPGEDKVRPACQHK 360	
Db	301	MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTVRVILLNWCWFLMKRPGEDKVRPACQHK 360	
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGPRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420	
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGPRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420	
Qy	421	LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVDRCLCLMAFSVFTI 480	
Db	421	LHGGOPPEGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVDRCLCLMAFSVFTI 480	
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	
RESULT 3			
A57175			
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004			
C:Accession: A57175			
R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.			
Genomics 26, 399-402, 1995			
A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine recept			
A:Reference number: A57175; MUID:95324936; PMID:7601470			
A:Accession: A57175			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-502 <ORR>			
A:Cross-references: UNIPROT:P49582; UNIPARC:UPI00002350D; GB:L37663; NID:g790853; PIDN:1			
C:Superfamily: acetylcholine receptor			
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;			
F:1-23/Domain: signal sequence #status predicted <SIG>			
F:224-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predic			
F:231-254/Domain: transmembrane #status predicted <TR1>			
F:262-280/Domain: transmembrane #status predicted <TR2>			
F:296-317/Domain: transmembrane #status predicted <TR3>			
F:470-488/Domain: transmembrane #status predicted <TR4>			
F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted			
F:415/Binding site: phosphate (Thr) (covalent) #status predicted			
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted			
Query Match 94.2%; Score 2545; DB 2; Length 502;			
Best Local Similarity 93.8%; Pred. No. 4.7e-207;			
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;			
Qy	6	GGVWLAAALAAASLLHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSLQIMDV 65	
Db	6	GGVWLAAALAAALHVSLOGEFQRLKYLKELVKVNYNPLERPVANDSQPLTVYFSLSLQIMDV 65	
Qy	66	DEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADERPAT 125	
Db	66	DEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIKWPDILLYNSADERPAT 125	
Qy	126	FHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDLQMOEA 185	
Db	126	FHTNVLVNSSGHCOYLPPGIFPKSCYIDVRWFPDVOHCKLKFGSWSYGWSLIDLQMOEA 185	
Qy	186	DISGYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245	
Db	186	DISSYIPNGEWDLVGIPGKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245	
Qy	246	ALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305	
Db	246	ALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305	

QY 306 LSVVTVTVLVQYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHKORRCS 365
DB 306 LSVVTVTVLVRYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHKORRCS 365

- QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVPTPDSGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDSGVVCGRLACSPTHDEHLHGHTH 425

QY 426 PPEGDPDLAKILLEEVRYIANRFRCDSEAVGSEWKFACVVDRLCLMAFSVFTIICITG 485
DB 426 PSDGDPDLAKILLEEVRYIANRFRCDSEVICSSEWKFACVVDRLCLMAFSVFTIICITG 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 4
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01378
R:Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
A:Reference number: Z14310; MUID:93147931; PMID:7678957
A:Accession: T01378
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: UNIPROT:Q05941; UNIPARC:UPI0000125244; EMBL:S53987; NID:G264770; PID:
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 93.6%; Score 2531; DB 2; Length 502;
Best Local Similarity 93.4%; Pred. No. 7.1e-206;
Matches 464; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 6 GGWTLAALASLHVSLSQGEFQRLKYLKYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGWTLAALASLHVSLSQGEFQRLKYLKYNPLERPVANDSQPLTVYFSLSLQIMDV 65

QY 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNSADERFDAT 125
DB 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNSADERFDAT 125

QY 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDYRWPFDPVQHCKLFGSWSYGSNLDLQMQEA 185
DB 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDYRWPFDPVQHCKLFGSWSYGSNLDLQMQEA 185

QY 186 DISGYIPNGEWDLVGIPGKRSEPFYECCKEPPDVTFTVMRRRLTYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEPFYECCKEPPDVTFTVMRRRLTYGLNLLIPCVLIS 245

QY 246 ALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASMTIIVG 305
DB 246 ALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASMTIIVG 305

QY 306 LSVVTVTVLVQYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHKORRCS 365
DB 306 LSVVTVTVLVRYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHKORRCS 365

QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVPTPDSGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDSGVVCGRLACSPTHDEHLHGHTH 425

QY 426 PPEGDPDLAKILLEEVRYIANRFRCDSEAVGSEWKFACVVDRLCLMAFSVFTIICITG 485
DB 426 PSDGDPDLAKILLEEVRYIANRFRCDSEVICSSEWKFACVVDRLCLMAFSVFTIICITG 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 5
JN0113
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JN0113; JH0172; S28018; B25738; S26566
R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.;
Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally
A:Reference number: JN0113; MUID:9107796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <COU>
A:Cross-references: UNIPROT:P22770; UNIPARC:UPI0000125243; GB:X68586; NID:G287756; PIDN:
A:Experimental source: white leghorn; brain
R:Schoppa, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-502 <SCH>
A:Cross-references: UNIPARC:UPI0000125243; EMBL:X52295; NID:G63077; PIDN:CAA36543.1; PID:
A:Experimental source: brain
R:Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.
EMBO J. 11, 4529-4538, 1992
A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter de
A:Reference number: S28018; MUID:93049204; PMID:1425587
A:Accession: S28018
A:Molecule type: DNA
A:Residues: 1-18 <NAS>
A:Cross-references: UNIPARC:UPI0000171278; EMBL:X68246; GB:S49751; NID:G65319; PIDN:CAA4
A:Experimental source: white leghorn; erythrocyte
R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Ra
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 'E', 28-41, 'X', 43-45, 'X', 47 <CON>
A:Cross-references: UNIPARC:UPI0000177976
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predic
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-485/Domain: transmembrane #status predicted <TR4>
F:46.90.133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:365.367.413.427.465/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 89.9%; Score 2429; DB 2; Length 502;
Best Local Similarity 90.7%; Pred. No. 3e-197;
Matches 449; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 8 VWLALASLHVSLSQGEFQRLKYLKYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67
DB 8 LWLALASLHVSLSQGEFQRLKYLKYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67

QY 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNSADERFDATFH 127
DB 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNSADERFDATFH 127

QY	128	TNVLNSSGHCQYLPPGIPKSSCYIDVRWFPDVOHQCKLKFGSWSYGGWSLDLQOEADI	187
Db	128	TNVLNSSGHCQYLPPGIPKSSCYIDVRWFPDVOHQCKLKFGSWSYGGWSLDLQOEADI	187
QY	188	SGYIPNGEWDLVGIPGKRSERYECCKEPYPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247
Db	188	SGYIPNGEWDLVGIPGKRTSEYECCKEPYPDITFTVMRRRTLYYGLNLLIPCVLISAL	247
QY	248	ALLVFLPADSGEKISLGIITVLLSTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS	307
Db	248	ALLVFLPADSGEKISLGIITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS	307
QY	308	VVTVIVLQYHHDPDGGKMPKWTVRVILLNCAWFLMRKRPGEDEVKVRPACQHKQRCSLA	367
Db	308	VVTVIVLQYHHDPDGGKMPKWTVRVILLNCAWFLMRKRPGEDEVKVRPACQHKQRCSLS	367
QY	368	SVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLHGQPP	427
Db	368	SMEMNTVSGQCSNGNLLYIGRGLDGVHCVPTPDGSGVICGRMTCSPTEENLLHSGHPS	427
QY	428	EGDPLAKLIEVRVRIANFRFCQDESEAVCSWEKFAACVVDRLCLMAFSVFTIICIGIL	487
Db	428	EGDPLAKLIEVRVRIANFRDQDEEALCNKWKFAASVVDRLCLMAFSVFTIICIGIL	487
QY	488	MSAPNFVEAVSKDFA 502	
Db	488	MSAPNFVEAVSKDFA 502	
RESULT 6			
JH0173			
Alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken			
C:Species: Gallus gallus (chicken)			
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004			
C:Accession: JH0173			
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.			
Neuron 5, 35-48, 1990			
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal subtypes of this			
A:Reference number: JH0173; MUID:90315158; PMID:2369519			
A:Accession: JH0173			
A:Molecule type: mRNA			
A:Residues: 1-511 <SCH>			
A:Cross-references: UNIPROT:Q03481; UNIPARC:UPI00000FB9BB; GB:X52296; NID:963081; PIDN:Q			
A:Experimental source: brain			
A>Note: this sequence is similar to acetylcholine receptor alpha chains			
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend			
C:Superfamily: acetylcholine receptor			
C:Keywords: glycoprotein; transmembrane protein			
F:1-30/Domain: signal sequence #status predicted <SIG>			
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AB			
F:239-263/Domain: transmembrane #status predicted <TM1>			
F:270-288/Domain: transmembrane #status predicted <TM2>			
F:304-323/Domain: transmembrane #status predicted <TM3>			
F:479-496/Domain: transmembrane #status predicted <TM4>			
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 67.2%; Score 1816.5; DB 2; Length 511;			
Best Local Similarity 68.8%; Pred. No. 1.7e-145;			
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;			
QY	8	WLAAASLLHVSLOGEQFKRLYKELVKNYNPLERPVANDSQPLTYVYFSLSLQIMDYDE	67
Db	16	LWASLFLSFFKVSQGESQRLLYRDLNRYNRLERPVANDSQPIVVELQLSLQIIDVDE	75
QY	68	KNQVLTNWLQMSWDHYLQNVSEYPGVKTVRPDQGIWKPDILLVNSADERDATFHT	127
Db	76	KNQVLTNWLQMYVDIYLSWDQYEYFGVQNLRFPSDQIWWPDILLVNSADERDATFHT	135
QY	128	TNVLNSSGHCQYLPPGIPKSSCYIDVRWFPDVOHQCKLKFGSWSYGGWSLDLQOEADI	187
Db	136	TNVLNYSGCCQYIIPGLIKSTCYIDVRWFPDVOHQCKLKFGSWSHGLDLQMLEADI	195
QY	188	SGYIPNGEWDLVGIPGKRSERYECCKEPYPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247

Db	196	SNYISNGEWDLVGVGKKNELYECCKEPYPDVTFTVMRRRTLYYGLNLLIPCVLISGL	255
QY	248	ALLVFLPADSGEKISLGIITVLLSTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS	307
Db	256	ALLVFLPADSGEKISLGIITVLLSTVFMLLVAEIMPATSDSVPLIAQYFASIMIVGLS	315
QY	308	VVTVIVLQYHHDPDGGKMPKWTVRVILLNCAWFLMRKRPGEDEVKVRP--QRRK	364
Db	316	VVTVIVLQYHHDPQAGKMPRWVRVILLNCAWFLMRKMPGEN--IKPLSKSYYPKHP	374
QY	365	SIASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLHG	424
Db	375	SLKNTMNVLPCHOPSGNMIY--SYHTMENPCPNNDLGSKGKITCPLSEDEHVKQK	433
QY	425	QPPEGDPLAKLIEVRVRIANFRFCQDESEAVCSWEKFAACVVDRLCLMAFSVFTIIC	484
Db	434	ALMDTIPVIVKLIEVQFIAMRFKQDGEIECSWEKFAAAVVDRLCLVAFTLFAICTF	493
QY	485	GILMSAPNFVEAVSKDF 501	
Db	494	TILMSAPNFIEAVSKDF 510	
RESULT 7			
S68588			
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis e			
C:Species: Caenorhabditis elegans			
C>Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004			
C:Accession: S68588; S57496			
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.			
J. Mol. Biol. 258, 261-269, 1996			
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.			
A:Reference number: S68587; MUID:96196478; PMID:8627624			
A:Accession: S68588			
A>Status: nucleic acid sequence not shown			
A:Molecule type: mRNA			
A:Residues: 1-498 <BAL>			
A:Cross-references: UNIPROT:P48180; UNIPARC:UPI0000125225; EMBL:X83887; NID:g872087; PID			
C:Superfamily: acetylcholine receptor			
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT>			
Query Match 41.0%; Score 1107.5; DB 2; Length 498;			
Best Local Similarity 44.6%; Pred. No. 1.4e-85;			
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;			
QY	10	LALAASLLHVSLOGEQF--RKLYKELVKNYNPLERPVANDSQPLTYVYFSLSLQIMDVDEK	68
Db	6	LLISCAILAAPTLGLSLQERRUYEDLMRYNRYNLERPVANHSEPVTVHLKVALQIIDVDEK	65
QY	69	NOVLTNWLQMSWDHYLQNVSEYPGVKTVRPDQGIWKPDILLVNSADERDATFHT	128
Db	66	NOVVVYNAWLDYTNWYDNLVWDKAEYGNITDVRFPAGKIWKPDVLLVNSVDTNFDSTYQT	125
QY	129	NVLNSSGHCQYLPPGIPKSSCYIDVRWFPDVOHQCKLKFGSWSYGGWSLDLQOEAA--D	186
Db	126	NWIVSTGLVNWVPPGIPKISKIDIQWFPDQKCFKFGSWTYDGYKLDLQAPATGCFD	185
QY	187	ISGYIPNGEWDLVGIPGKRSERYECCKEPYPDVTFTVMRRRTLYYGLNLLIPCVLISA	246
Db	186	ISEYISNGEWALPLTTVERNEKFYDCCPEPYDPVHFVFLHMRRTLYYGFNLIMPICILTTL	245
QY	247	LALLVFLPADSGEKISLGIITVLLSTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGL	306
Db	246	MTLLGLFTLPDAGEKITLIQITVLLSICFFLSIVSEMSPTSEAVPLLIIGFIFFCCMIVVTA	305
QY	307	SVWTVIVLQYHHDPDGGKMPKWTVRVILLNCAWFLMRKRPGEDEVKVRPACQHKQRCSL	366
Db	306	STVTVVIVNLHYRTPETHDMPWRNLLVLLWIPIELMKRPG-----HNLTYASL	356
QY	367	ASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDS-----GVVCGRMAC	412

Db 357 PSL-----PSTKNRHSSESIRNIK--DNEHSLSRANSPDQCLNQYIMTQSVNSGLTSL 410
QY 413 SPTHDEHLHGQPPGDDP-----LAKILEVRYIANRFRQDSEAVCSWKAACV 467
Db 411 GSIPSTMISNGTTDVSQAATLLILRIYHELKIVTKRMIBGDKBEQACNNKFAAMV 470
QY 468 DRLCMARSVFTICTIGILMSAPNV 494
Db 471 DRCLYVFTIFIVSTIGIFWAPYLV 497

RESULT 8

T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: UNIPROT:O62083; UNIPARC:UPI000017799E; EMBL:Z93778; PIDN:CAB07843.1;
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.3%; Score 1089.5; DB 2; Length 560;
Best Local Similarity 40.6%; Pred. No. 5.3e-84;
Matches 226; Conservative 93; Mismatches 157; Indels 81; Gaps 9;

QY 10 LALAASLL-----HVSIGQEFQRLYKELVKNYNPLRPVANDSQPTVYFSLSLQI 62
Db 8 LVLVSILIWETKCSKVIWTDHERRLYAKLAENYKLRPVNRESEAVVVLGGHDYQOI 67
QY 63 MDVDEKQVLTNNILQMSWTDHYLQWNVSEYPGVKTVFPDQIQWKPDIILYNSADERP 122
Db 68 LDIDEHQIMNENWLMRWGTDHYLTWDESEFNGIKVEKRLPINNWKPDLVLYNSVDQOF 127
QY 123 DATFTNNVLVNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCCLKFGWSYGGWSLDLQ 182
Db 128 DSTWPNVAVLYTGNVTWIPPAIRSSCAIDYAFPDQHCCTMKFGSWTYSGFDTLIN 187
QY 183 QEADISGYTPNGEWDLVGIPGRSERPYECCKEPPDVTFTVTRRTLYYGNLLIPCV 242
Db 188 TTISPATYKPNGEWELLGLTSQISIPFYECCEPEYVDVFTVSIRRTLYYGNLLPCW 247
QY 243 LLSALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYASTMI 302
Db 248 LLSALLSFTLPADGGEKLNIGVTFMSLCFMIMVAEMPQTSALPLIQIYSCIMF 307
QY 303 IVGLSVVTVIVLYQHHPDGGK-MPKWTRVILLNWCWFLMRKRPGRDKVRPACQH--- 359
Db 308 QVGASVATVIALNFHRSPEQYKPNKFKTLKLLGWLPTLGMERPDLVLELSVGHAY 367
QY 360 ----KORCSLASVEMSAVAPPASNGNLLYIGFRGLD----- 393
Db 368 SDNKKQRYLIEVERHILTRP---NGN---GHSADVKAHVLDLSTGNPHSDAKKSSPS 420
QY 394 -----GVHCVPFP-----DSGV---VCGRMACSPTHDEHLLHGQPPGDP---- 431
Db 421 PKRTSASIMGWTLPTQMGALDGSINKYCTKTVRPLENGSATINHKSSPQIPINN 480
QY 432 -----DLAKILEVRYIANRFRQDSEAVCSWKAACVVDRLCLMAF 475
Db 481 NIYKCANNOKTOPEDRHFHILNELRVISARVRKEEMHALQDMWFASVRDVRVCF 540

QY 476 SVFTIICTIGILMSAPN 492
Db 541 SAFLFWCTAILSYNAPH 557

RESULT 9

T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: UNIPROT:P91197; UNIPARC:UPI0000061185; EMBL:U88167; PIDN:AAB42223.1;
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 36.9%; Score 998; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 2.2e-76;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

QY 12 LAASLLHVSLL-QGEF-QRKLYKELVKNYNPLRPVANDSQPTVYFSLSLQIMDVDEKN 69
Db 10 LSLVITHSNLCDSVAETKLTDDLKGNPLRPVQNSQPLEVKIKLFLQQLLDVDEKN 69
QY 70 QVLTNNILQMSWTDHYLQWNVSEYPGVKTVFP--DGOIWKPDILLYNSADERDATEPH 127
Db 70 QIVSVNWLSTYTFWPKLQWEPKKYGGIQDIRPQSSDHIWKPDVLLYNSAAEDFDSTFK 129
QY 128 TNNVLVNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCCLKFGWSYGGWSLDLQ----- 182
Db 130 SNLLTYHTGTVMVIPPGLKFCVQLDVTWFPDDQVCEMKFGSWTFHGYAIDQLDDDTN 189
QY 193 --QEADISGYTPNGEWDLVGIPGRSERPYECCKEPPDVTFTVTRRTLYYGNLLIP 240
Db 190 GTQSDMLSTYLVNGSQWISTNAKRVSYKCCPEPYTVNTYLHRRRTLYYGNLLIP 249
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 250 SLLISLMAILGPMFPDAGEKITLLEVTLILAIVFPLSWSEMTPTSEAVPLIGVFFSCC 309
QY 301 MIIVGLSVVTVIVLYQHHPDGGKMPKWKTRVILLNWCWFLMRKRPGEDEKVRPACQHK 360
Db 310 MLVVSASVFTIVTLNLHFRSADSHENMPLVRVLEFLPMLLFMSRPGYKFKV----- 363
QY 361 QRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVTP-TPDSGVVCGRMACSPTHDEH 419
Db 364 -----ANV-----IDSTDKMPKKPKNPLDCLNPLNHNHAGYEAQ 395
QY 420 LHHGQPPGDDPLAKILEEVRYIANRFRQDSEAVCSWKAACVVDRLCLMAFVSFT 479
Db 396 ILL-----LHSHVTELRRVAVTFNKEBDEHRIQTDWRFAAMVVDRACLLLFTVFI 445
QY 480 ICTICTIGILMSAPNV 494
Db 446 VISILAIMMSAPHII 460

RESULT 10

S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S12359
R:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBL J. 9, 4391-4398, 1990
A:Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic A:Reference number: S12359; MUID:91092263; PMID:1702381
A:Accession: S12359
A:Molecule type: mRNA
A:Residues: 1-557 <NAR>
A:Cross-references: UNIPROT:P23414; UNIPARC:UPI0000125229; EMBL:X55439; NID:g10133; PIDN C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein F:1-23/Domain: signal sequence #status predicted <SIG>
F:245-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <NAR>
F:245-266/Domain: transmembrane #status predicted <TM1>
F:274-295/Domain: transmembrane #status predicted <TM2>
F:308-329/Domain: transmembrane #status predicted <TM3>
F:501-523/Domain: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 35.0%; Score 947; DB 2; Length 557;
Best Local Similarity 37.1%; Pred. No. 5.8e-72;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGVWLAALASLLHVSLOGEFQKLYKELVKYNPLERPVANDSOPLTYYFSLSLQIMD 64
Db 6 PPMLELLLLLLHHPAAANPDARLYDILLSNYNRLIRPVSNNTDTVLVGLGLSLQSLID 65
QY 65 VDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGGQIKWPDILLVNSADFERDA 124
Db 66 LNLKQDILTTNWLSHEWQDKFRWDPAEYGVGTLYVPSEHILWPDVLVYNADGEYV 125
QY 125 TPTHNLVNSGHCQYLPPIGFKSSCYIDVRWFPDVQHKCLKFGWSYGGWSLDLQ--- 181
Db 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDRVYFPDQTCFWMKFGSWYDGDQIDLKHN 185
QY 182 -----MQEADISGYTPNGEWDLVGPGRSERFYCCCKEPPDVFTVTMRRTLYY 233
Db 186 QKYDDNKVKVGIDLEYPSPVEWDLGVPAPERHEKYPCCAEPYDIPFNFTLRKRTLYF 245
QY 234 GLNLIPCVLISALALLVFLPADSGEKISIGITVLLSLTTFMLIVARIMPATSDSVPLI 293
Db 246 TVNLIVPCUGISYLSLVFYLPADSGEKIALCISILLSTQTFWFLISIIISTSLALFLL 305
QY 294 AQYFASTMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRGE--- 350
Db 306 GKYLFTWLVGLSVITIMVLNVHYRKPSTHKMAPVYKVFIRLPKLLMRVPEQLA 365
QY 351 DKVRPACQHKORRCSLASVMSAVAPPPASNGNLLIYIGFRGLDGVHCVPPTDPSGVVCGRM 410
Db 366 DLASKRLLRHANHSKLSAAAAAATAAASS-----AASSPDS--LRHH 408
QY 411 ACSPTHDEHL-LHGGQPPG----- 429
Db 409 LHQHQHQHLLQHLHQRPQGGNGLHSATNRRGGSAGAGGLPSVVGLDGSLSVATRKYY 468
QY 430 DPDLAKILEEVRYIANRRCODESEAVCSWKFAACVVDRLCLMAFSVFTIICITIGILMS 489
Db 469 PFELEKAHNVLFIQNHMQRQDEFFDAEDQDQGFVAVWLDRLFLWIFTIASIVGIFAILCE 528
- QY 490 AP 491
Db 529 AP 530

- RESULT 11
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188

A:Accession: T19862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: UNIPROT:Q18556; UNIPARC:UPI000007DC28; EMBL:Z70266; PIDN:CAA94206.1;
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 495/
C:Superfamily: acetylcholine receptor

Query Match 34.9%; Score 944; DB 2; Length 542;
Best Local Similarity 37.7%; Pred. No. 1e-71;
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;

QY 11 ALAASLLHV-----SLOGEFQKLYKELVKYNPLERPVANDSOPLTYYFSLSLQIMDV 65
Db 12 ALHCVLFHLLTEVHSSADEY--RLLDLRHNDPYRVPVANAPEPLVSVKYLQOILDV 69
QY 66 DEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRPPD--GQIWKPDILLVNSADERFD 123
Db 70 DEKQVITLVAVIEFYQWTDYKLKWDPSYGGIKDIRIPGNANAIWKPDVLLVNSADENFD 129
QY 124 ATFTHTNLVNSGHCQYLPPIGFKSSCYIDVRWFPDVQHKCLKFGWSYGGWSLDLQ-- 182
Db 130 STYFVNVVSYTGDVLQVPPGILKLSCKIDITYPPDDQICHLKFGSWYSGNFIDLRIN 189
QY 183 -----QEADISGYTPNGEWDLVGPGRSERFYCCCKEPPDVFTVTMRRTLYY 233
Db 190 GPEGKNSDEGIDVOYYVQNGEWNLLAVPARHETNIFD--EQYPSLEFFYLIIQRTLYY 247
QY 234 GLNLIPCVLISALALLVFLPADSGEKISIGITVLLSLTTFMLIVARIMPATSDSVPLI 293
Db 248 GLNLIPFLLISLMTVLGFTLPDAGEKITLEIITLLSVCFSLSVADMTPTSEAVPLI 307
QY 294 -----AQYFASTMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKR 347
Db 308 GLIIFSGAFFSCCLMVVSASVVFVTLVNLNHRKPETHMSPFRLLELLIWLPMLLMR 367
QY 348 PGEDKVRPACQHKORRCSLASVMSAVAPPPASNGNLLIYIG-FRGLDGVHCVPPTDSG-- 404
Db 368 PG--KTFNCTHLKAEKAEKAKQGS-----KNG-----VGPGRPTDSVH-----PSEGLS 412
QY 405 -----VVCGR-MACSPTHDEHLHGG-----QPEGDP----- 431
Db 413 LMKIKLGRQQTIDFEYEFVQHNLMPVASEMTPVTVYSKVMASVEDVVMTELNY 472
QY 432 -----DLAKILEEVRYIANRRCODESEAVCSWKFAACVVDRLCLMAFSVFTIICITIG 485
Db 473 MQKACLELKNISSQTRAMRKMEDEDERDEQAANDKFAAMVVDRCCLITFSVFIVVSTCG 532
QY 486 ILMSPAPNV 494
Db 533 IMFSSPHLI 541

RESULT 12
A40110
nicotinic acetylcholine receptor alpha-2 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C:Accession: A40110
R:Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson, L.
Science 240, 330-334, 1988
A:Title: Functional expression of a new pharmacological subtype of brain nicotinic acetyl A:Reference number: A40110; MUID:88178113; PMID:2832952
A:Accession: A40110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <WAD>
A:Cross-references: UNIPROT:P12389; UNIPARC:UPI0000170855; GB:M20297; NID:g202672; PIDN: A:Note: the authors translated the codon TCG for residue 494 as Cys

C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 34.9%; Score 942.5; DB 2; Length 511;
Best Local Similarity 39.0%; Pred. No. 1.2e-71;
Matches 201; Conservative 83; Mismatches 179; Indels 53; Gaps 9;

QY 8 VW--LALASLLHVSLOGEFORKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIMDV 65
DB 16 LMCLLVPAVLTOQGSHTHAERDLFKHLFGGYNRWARPVNTSDVIVRFGLSIAQLIDV 75
QY 66 DEKNQVLTNTIWLQMSWTDHYLQWNSYEPYGVKTVRFPDQIQWKPDILLYNADSEDFAT 125
DB 76 DEKNQVMTTNVWLKQWANDYKLRWDPAEFGNTVSLRVPSEMIWIPDIVLYNNADGEFAT 135
QY 126 FHTNVLVNSSGHCQYLPPIGFIKSSCYIDVRVFPFVQHCKLFGWSYSGWSLDLQMOB- 184
DB 136 HMTKAHLPTGTVHWVPPAIYKSSCSIDVTFPPFQDQCKMKFGSWTYDKAKIDLEQMBR 195
QY 185 -ADISGYIPNGEWDLVGIPGKSERFYECKEPPYDVTFTVMRRRTLYYGLNLLIPCVL 243
DB 196 TVDLKDYWSGMAWINATGTYNSKKYCCAIYPDVTYFYFIRRLPLEYTNLIIPCLL 255
QY 244 ISALALLVPLPADSGEKISLGIITVLLSLTTFMLLVABIMPATSDSVPLIAQVFASTMI 303
DB 256 ISCLTVLVYLSGCEGKILCISVLLSLTVFLLLTITLIPSTLSVPLIGIYLLFTMLP 315
QY 304 VGLSVVTVIVLYQHHDHDPGGKMPKWTTRVILLNMCWFLRMKRP-----GEDKVRPA 356
DB 316 VTLSIVTVFVLNVHRSSTHNPWNVVALLGRVPRWLMMNRPLPPMELHSGSPDLKLS 375
QY 357 COHQKQRCSLASVEMSAVAPPASNGNLYIGRGLDGVHCYVTPDSS--GVVCGRMASCP 414
DB 376 PSYHMLETNDAGERETEBEEEDENICV-----CAGLDSSMGVLYG----- 420
QY 415 THDEHLLHGS-----QPPGSG-----DPLAKILEEYRYIANRFRCDSEAVCS 458
DB 421 -----HGLHLRAMEPTKTPSQASEILLSPQKALEGVHYIADRURSDADSSVKE 473
QY 459 EWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
DB 474 DMKYVAVVDRFLWLFIIIVSLFTIGLFL--PPFL 507

RESULT 13

S14703
nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)
C:Species: Carassius auratus (goldfish)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S14703
R:Hiieber, V.; Bouchev, J.; Agranoff, B.W.; Goldman, D.
Nucleic Acids Res. 18, 5307, 1990
A:Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic acetylcholine receptor
A:Reference number: S14703; MUID:90384858; PMID:2402468
A:Accession: S14703
A:Molecule type: mRNA
A:Residues: 1-459 <HIE>
A:Cross-references: UNIPROT:P19370; UNIPARC:UPI0000125260; EMBL:X54052; NID:g62576; PIDN
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

Query Match 34.7%; Score 938.5; DB 2; Length 459;
Best Local Similarity 38.5%; Pred. No. 2.4e-71;
Matches 189; Conservative 95; Mismatches 142; Indels 65; Gaps 8;

QY 35 KYNPLRPVANDSQPLTYVYFSLSLQIMDVDEKQVLTNTIWLQMSWTDHYLQWNSY 94
DB 10 ERYNKLIRPAVNSQVQVITGIKLSLAQLISVNEREQIMTNTYMLTQSWTDYDLVNDPNEY 69
QY 95 PGVKTVPDGOIKWPKDILLYNADSEDFATHTNVLVNSSGHCQVLPPIGFIKSSCYIDV 154
DB 70 EGKIKLIRPISQHLWLPDIVLYNNADGVYEVSYCNVAVSNTGDIPLWLPPIYKSAIEV 129

QY 155 RWFPEDVOHCKLFGWSYSGWSLDQMOE--ADISGYIPNGEWDLVGIPGKSERFYEBC 212
DB 130 RNFPEDQONCTLKFRSWTYIDTELDLVTSDFASRDDTTPSGEWDIVSLPGRKNE----- 184
QY 213 CKEP-----YPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGI 268
DB 185 --DPNDLTVDITDVFVIRKRPFPYTNLIIPCVLITSLATLVFLYLPSPDCGSEKVTLCMSV 242
QY 269 LLSLTTFMLLVABIMPATSDSVPLIAQVFASTMIIVGLSVVTVIVLYQHHDHDPGGKMP 328
DB 243 LLALTVFLLLSKIVPPTSLAVPLIGKYLMTVLTWLTFTSIVTSVCLVNVHRSRSPSTHMP 302
QY 329 KWTRVILLNMCWFLRMKRPCEDEKVRPAQCOHKQRCSLASVEMSAVAPPASNGNLLIYIG 388
DB 303 EMVKCVFLHKLPAFLMRPGRSNVRFRKQKHSFSSHQ----- 344
QY 389 FRGLDGVHCYVTPDSSGVVCGRMASCPTHDEHLLHGGQPPG-----DPLAKIL 437
DB 345 ---DGDSPFLTDDPGRVCGARV-----GDLPEGSEPRQVRKVRHDDQVDDEAI 389
QY 438 BEVRYIANRFRCDSEAVCEWKPAAACVDRCLCMASFVFTIICITIGILMSAPNF----- 493
DB 390 DGVRFIAHMKIEDDEGIIEDMKYVAMVIDRLFLWIFILVCVVGTLGLFVQ-PLFQSYN 448
QY 494 ---VEAVSKDP 501
DB 449 TPVABEYVGD 459

RESULT 14

ACCH2N
nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00377
R:Nef, P.; Oneyaer, C.; Alliod, C.; Couturier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A:Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptor subunit families
A:Reference number: S00376; MUID:88283624; PMID:3267226
A:Accession: S00377
A:Molecule type: DNA
A:Residues: 1-528 <NEF>
A:Cross-references: UNIPROT:P09480; UNIPARC:UPI000012522D; EMBL:X07339; NID:g62792; PIDN

C:Genetics:

A:Introns: 21/1; 73/3; 88/3; 125/2; 487/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
F:241-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-327/Domain: transmembrane #status predicted <TM3>
F:502-520/Domain: transmembrane #status predicted <TM4>
F:54.104/Binding site: carbohydrate (Aen) (covalent) #status predicted
F:158-172,222-223/Disulfide bonds: #status predicted

Query Match 34.7%; Score 937.5; DB 1; Length 528;
Best Local Similarity 37.8%; Pred. No. 3.4e-71;
Matches 200; Conservative 85; Mismatches 175; Indels 69; Gaps 10;

QY 8 VWLAL---AASLLHVSLOGEFORKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIMD 64
DB 13 VMCFTVLTQANTREQQPHGFADRLFKHLFTGYNRWSRPVNTSDVIVKFGLSIAQLID 72
QY 65 VDEKNQVLTNTIWLQMSWTDHYLQWNSYEPYGVKTVRFPDGOIKWPKDILLYNADSEDFDA 124
DB 73 VDEKNQVMTTNVWLKQWANDYKLRWDPAEFGNTVSLRVPSEMIWIPDIVLYNNADGEFV 132
QY 125 TFHTNVLVNSSGHCQVLPPIGFIKSSCYIDVRVFPFVQHCKLFGWSYSGWSLDLQMOB 184
DB 133 THMTKAHLFSGKVKVWVPPAIYKSSCSIDVTFPPDQCKMKFGSWTYDKAKIDLENNE 192
QY 185 --ADISGYIPNGEWDLVGIPGKSERFYECKEPPYDVTFTVMRRRTLYYGLNLLIPCV 242


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Db      361  QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy      421  LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
Q5W554 HUMAN
ID Q5W554_HUMAN PRELIMINARY; PRT; 502 AA.
AC Q5W554;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Nicotinic acetylcholine alpha-7 subunit.
GN Names=CHRNA7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Brues M., Bonisch H., Gothert M.;
RT "Modulatory cannabinoid effects at recombinant homomeric human
RT nicotinic acetylcholine alpha-7 receptors.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Brues M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AJ586911; CAE52911.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_chan_LBD.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_Channel_memb.
DR InterPro; IPR002394; Nic/ace_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Transmembrane;
KW Transport.
SQ SEQUENCE 502 AA; 56503 MW; 235F80F38FB50F46 CRC64;

Query Match 99.4%; Score 2688; DB 2; Length 502;
Best Local Similarity 99.4%; Pred. No. 5.5e-212;
Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Db      1  MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSL 60
Qy      61  QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPDGIWKPDILLYNSADE 120

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Db      61  QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVPDPDGIWKPDILLYNSADE 120
Qy      121  RPDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVWFFDVQVCKLKFGSWSYGGWSLDL 180
Db      121  RPDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVWFFDVQVCKLKFGSWSYGGWSLDL 180
Qy      181  QMQEADISGYIENGWDLVGIPGKSERFYECKEPYDPDVTFTVMRRRTLYGLNLLIP 240
Db      181  QMQEADISGYIENGWDLVGIPGKSERFYECKEPYDPDVTFTVMRRRTLYGLNLLIP 240
Qy      241  CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPIAQYFAST 300
Qy      301  MIIVGLSVVVTVIVLYHHDDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRPACQHK 360
Db      301  MIIVGLSVVVTVIVLYHHDDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRPACQHK 360
Qy      361  QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db      361  QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy      421  LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
ACHA7_MACHU
ID ACHA7_MACHU STANDARD; PRT; 502 AA.
AC Q866A2;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN Name=CHRNA7;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=14764638; DOI=10.1210/en.2003-1728;
RA Prokocil B.J., Sekhon H.S., Jia Y., Savchenko V., Blakely R.D.,
RA Lindstrom J., Spindel R.R.;
RT "Acetylcholine is an autocrine or paracrine hormone synthesized and
RT secreted by airway bronchial epithelial cells.";
RL Endocrinology 145:2498-2506(2004).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane (By similarity).
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; AF486623; AA084497.1; -; mRNA.
DR HSSP; P22770; 1KL8.
DR InterPro; IPR006029; Neu_channel_memb.

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DR InterPro; IPR006202; Neur_chan_lig_bd.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR002394; Nic/ace_receptor.
DR PANTHER; PTHR18945; Neur_chan; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRICNCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Postsynaptic membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 502
FT
FT TOPO_DOM 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT TOPO_DOM 318 469
FT TRANSMEM 470 490
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT DISULFID 150 164 By similarity.
FT DISULFID 212 213 Associated with receptor activation (By similarity).
FT SEQUENCE 502 AA; 56429 MW; 213C8A282242AC4A CRC64;

Query Match 99.0%; Score 2675; DB 1; Length 502;
Best Local Similarity 98.8%; Pred. No. 6.5e-211;
Matches 496; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAALASLLHVSLOGEFQRLYKELVKNYNPLRPVANDSQPLTVVPSLSLL 60
Db 1 MRCSPGGWLAALASLLHVSLOGEFQRLYKELVKNYNPLRPVANDSQPLTVVPSLSLL 60
QY 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNIWLQMSWDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
QY 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQCKLKFGSWSYGWSL 180
Db 121 RFDATFHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQCKLKFGSWSYGWSL 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKSEKPYECKEPPYDVTFTVTRRTLYYGLNLLIP 240
Db 181 QMOEADISGYIPNGEWDLVGIPGKSEKPYECKEPPYDVTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVLLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVLLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIIVGLSVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPCGEDKVRPACQHK 360
Db 301 MIIIVGLSVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPCGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHL 420
QY 421 LHGGQPPGDPDLAKLIEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKLIEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILSAPNFVEAVSKDFA 502
Db 481 ICTIGILSAPNFVEAVSKDFA 502
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RESULT 4
Q53YK2_RAT
_ID Q53YK2_RAT PRELIMINARY; PRT; 502 AA.

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AC Q53YK2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha7 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Groot-Kormelink P.J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
DR EMBL; AY574256; AAS90352.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005236; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
SQ SEQUENCE 502 AA; 56502 MW; 289A30498C7B9A58 CRC64;

Query Match 94.2%; Score 2547; DB 2; Length 502;
Best Local Similarity 93.8%; Pred. No. 2.1e-200;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLALAAASLLHVSLOGEFQRLYKELVKNYNPLRPVANDSQPLTVVPSLSLLQIMDV 65
Db 6 GGVWLALAAASLLHVSLOGEFQRLYKELVKNYNPLRPVANDSQPLTVVPSLSLLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADERFPAT 125
Db 66 DEKNQVLTNIWLQMSWDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADERFPAT 125
QY 126 FHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQCKLKFGSWSYGWSLQMQEA 185
Db 126 FHTNVLVNSSGHCQYLPPIGFKSSCYIDVRWFFPDVQCKLKFGSWSYGWSLQMQEA 185
QY 186 DISGYIPNGEWDLVGIPGKSEKPYECKEPPYDVTFTVTRRTLYYGLNLLIPCVLLIS 245
Db 186 DISGYIPNGEWDLVGIPGKSEKPYECKEPPYDVTFTVTRRTLYYGLNLLIPCVLLIS 245
QY 246 ALALLVLLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALALLVLLPADSGEKISLGIITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPCGEDKVRPACQHKRRCS 365
Db 306 LSVVTVIQLYHHDDPGGKMPKWTTRVILLNWCANFLMRKPCGEDKVRPACQHKRRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHLHGQ 425
Db 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPDGSGVVCGRMACSPHDEHLHGQ 425
QY 426 PPEGDPDLAKLIEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485
Db 426 PPEGDPDLAKLIEEVRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485
QY 486 ILSAPNFVEAVSKDFA 502
Db 486 ILSAPNFVEAVSKDFA 502
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RESULT 5
Q9JHD6_MOUSE

ID	Q9JHD6_MOUSE PRELIMINARY; PRT; 502 AA.	Q9JHD6; 502 AA.
DT	01-OCT-2000 (T:EMBLrel. 15, Created)	01-OCT-2000 (T:EMBLrel. 15, Last sequence update)
DT	01-OCT-2000 (T:EMBLrel. 15, Last sequence update)	01-OCT-2000 (T:EMBLrel. 15, Last sequence update)
DT	01-JUN-2003 (T:EMBLrel. 24, Last annotation update)	01-JUN-2003 (T:EMBLrel. 24, Last annotation update)
DE	Nicotinic acetylcholine receptor subunit alpha 7.	Nicotinic acetylcholine receptor subunit alpha 7.
GN	Name=Chrna7;	Name=Chrna7;
OS	Mus musculus (Mouse).	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;	NCBI_TaxID=10090;
RN	[1]	[1]
RP	NUCLEOTIDE SEQUENCE.	NUCLEOTIDE SEQUENCE.
RC	STRAIN=DBA/21b3;	STRAIN=DBA/21b3;
RC	STRAIN=97189245; PubMed=9037516; DOI=10.1016/S0169-328X(96)00149-0;	STRAIN=97189245; PubMed=9037516; DOI=10.1016/S0169-328X(96)00149-0;
RA	Stitzel J.A., Farnham D.A., Collins A.C.;	Stitzel J.A., Farnham D.A., Collins A.C.;
RT	"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-bungarotoxin binding in brain."	"Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-bungarotoxin binding in brain."
RT	Brain Res. Mol. Brain Res. 43:30-40(1996).	Brain Res. Mol. Brain Res. 43:30-40(1996).
RN	[2]	[2]
RP	NUCLEOTIDE SEQUENCE.	NUCLEOTIDE SEQUENCE.
RC	STRAIN=DBA/21b3;	STRAIN=DBA/21b3;
RA	Scitzel J.A.;	Scitzel J.A.;
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC	-1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.	-1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
DR	EMBL; AF225980; AAF35885.1; -; mRNA.	EMBL; AF225980; AAF35885.1; -; mRNA.
DR	HSSP; P22770; 1KL8.	HSSP; P22770; 1KL8.
DR	MGI; MGI:99779; Chrna7.	MGI; MGI:99779; Chrna7.
DR	GO; GO:0005615; C:extracellular space; TAS.	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0016021; C:integral to membrane; TAS.	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0005515; P:protein binding; IPI.	GO; GO:0005515; P:protein binding; IPI.
DR	InterPro; IPR006201; Neur chan LBD.	InterPro; IPR006201; Neur chan LBD.
DR	InterPro; IPR006029; Neur channel memb.	InterPro; IPR006029; Neur channel memb.
DR	InterPro; IPR002394; Nic/ace receptor.	InterPro; IPR002394; Nic/ace receptor.
DR	Pfam; PF02931; Neur_chan_LBD; 1.	Pfam; PF02931; Neur_chan_LBD; 1.
DR	Pfam; PF02932; Neur_chan_memb; 1.	Pfam; PF02932; Neur_chan_memb; 1.
DR	PRINTS; PR00254; NICOTINIC.	PRINTS; PR00254; NICOTINIC.
DR	TIGRFAMs; TIGR00860; LIC; 1.	TIGRFAMs; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.	PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
KW	Ion transport; Ionic channel; Postsynaptic membrane; Receptor;	Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW	Transmembrane; Transport.	Transmembrane; Transport.
SQ	SEQUENCE 502 AA; 56617 MW; C9353B5136D620B3 CRC64;	SEQUENCE 502 AA; 56617 MW; C9353B5136D620B3 CRC64;
Query Match 94.2%; Score 2546; DB 2; Length 502;		
Best Local Similarity 93.8%; Pred. No. 2.6e-200; Gaps 0;		
Matches 466; Conservative 19; Mismatches 12; Indels 0		
Qy	6 GGYWLAALASLHVSILQGEFQRLKYLKYNPLERPVANDSPLTYVFSLSLIQMDV 65	6 GGYWLAALASLHVSILQGEFQRLKYLKYNPLERPVANDSPLTYVFSLSLIQMDV 65
Db	6 GGIWLAALAAHLSVLSQGEFQRLKYLKYNPLERPVANDSPLTYVFSLSLIQMDV 65	6 GGIWLAALAAHLSVLSQGEFQRLKYLKYNPLERPVANDSPLTYVFSLSLIQMDV 65
Qy	66 DERKQVLTNNIWLQMSWTHYLVQNNVSEYVPGVKTVPDPGQIWKPDILLNSADERFAT 125	66 DERKQVLTNNIWLQMSWTHYLVQNNVSEYVPGVKTVPDPGQIWKPDILLNSADERFAT 125
Db	66 DERKQVLTNNIWLQMSWTHYLVQNNVSEYVPGVKTVPDPGQIWKPDILLNSADERFAT 125	66 DERKQVLTNNIWLQMSWTHYLVQNNVSEYVPGVKTVPDPGQIWKPDILLNSADERFAT 125
Qy	126 FHTNVLVNSGHCOYLPPIGFKSSCCYIDVRWPPDVORCKLFGSWSYGGSLDLQWQEA 185	126 FHTNVLVNSGHCOYLPPIGFKSSCCYIDVRWPPDVORCKLFGSWSYGGSLDLQWQEA 185
Db	126 FHTNVLVNSAGHCQYLPPIGFKSSCCYIDVRWPPDVORCKLFGSWSYGGSLDLQWQEA 185	126 FHTNVLVNSAGHCQYLPPIGFKSSCCYIDVRWPPDVORCKLFGSWSYGGSLDLQWQEA 185
Qy	186 DISGYIPNGEWDIVGIPGKRSEPFYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245	186 DISGYIPNGEWDIVGIPGKRSEPFYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245
Db	186 DISSYIPNGEWDIVGIPGKRSEPFYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245	186 DISSYIPNGEWDIVGIPGKRSEPFYECCKEYPDVFTVTWRRRTLYYGLNLLIPCVLIS 245
Qy	246 ALALLVFLIPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305	246 ALALLVFLIPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db	246 ALALLVFLIPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305	246 ALALLVFLIPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -|- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
 CC bungarotoxin. The structure is probably pentameric (By
 CC similarity).
 CC -|- INTERACTION:
 CC P05067:APP (xeno); NBExp=1; IntAct=EBI-79422, EBI-77613;
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
 CC family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; S53987; AAB25224.2; -; mRNA.
 CC EMBL; L31619; AAC33136.1; -; mRNA.
 CC PIR; T01378; T01378.
 CC RSP; P22770; 1KJ8.
 CC IntAct; Q05941; -.
 CC Ensembl; ENSRNOG0000010853; Rattus norvegicus.
 CC RGD; 2348; Chrna7.
 CC GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
 CC GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; IDA.
 CC InterPro; IPR006029; Neur channel memb.
 CC InterPro; IPR006202; Neur chan lig bd.
 CC InterPro; IPR006201; Neur channel.
 CC InterPro; IPR002394; Nic/ace receptor.
 CC PANTHER; PTHR18945; Neur_chan; 1.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan memb; 1.
 CC PRINTS; PR00254; NICOTINIC.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRFAMs; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
 KW Postsynaptic membrane; Signal; Transmembrane; Transport.
 FT SIGNAL 1 22 By similarity.
 FT CHAIN 23 502 Neuronal acetylcholine receptor protein,
 FT alpha-7 subunit.
 FT 23 230 Extracellular (Potential).
 FT TRANSMEM 231 255 Potential.
 FT TRANSMEM 262 280 Potential.
 FT TRANSMEM 296 317 Potential.
 FT TOPO_DOM 318 469 Cytoplasmic (Potential).
 FT TRANSMEM 470 490 Potential.
 FT CARBOHYD 46 46 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 90 90 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 133 133 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 150 164 By similarity.
 FT DISULFID 212 213 Associated with receptor activation (By
 FT similarity)
 FT CONFLICT 447 447 N -> F (in Ref. 2).
 FT CONFLICT 469 469 P -> R (in Ref. 2).
 SQ SEQUENCE 502 AA; 56410 MW; 00996E74EC7B9A56 CRC64;
 Query Match 93.6%; Score 2531; DB 1; Length 502;
 Best Local Similarity 93.4%; Pred. No. 4.4e-199;
 Matches 464; Conservative 18; Mismatches 15; Indels 0; Gaps 0;
 QY 6 GGWIALAASLHVSLSQGFQRKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
 Db 6 GGWIALAASLHVSLSQGFQRKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDV 65
 QY 66 DEKNQVLTNINLQNSWTDHYLQWNSVEYPGVKTVPDQGIWKPDILLYNSADRRPDAT 125
 Db 66 DEKNQVLTNINLQNSWTDHYLQWNSVEYPGVKNVRFPDQGIWKPDILLYNSADRRPDAT 125

QY 126 FHTNVLVNSSGHCQYLPGIFKSSCYIDVRPFPDVQHCCKLFGSGWSYGLDLQMQEA 185
 Db 126 FHTNVLVNSSGHCQYLPGIFKSSCYIDVRPFPDVQHCCKLFGSGWSYGLDLQMQEA 185
 QY 186 DISGYPNGEWDLVIGIPGRSRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIFCVLIS 245
 Db 186 DISSYPNGEWDLVIGIPGRSRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIFCVLIS 245
 QY 246 ALALVFLPADSGEKISLIGITVLLSTTFMLLVABIMPATSDSVPLIAQVFPASTMIIVG 305
 Db 246 ALALVFLPADSGEKISLIGITVLLSTTFMLLVABIMPATSDSVPLIAQVFPASTMIIVG 305
 QY 306 LSVVVTVIYVYHHDPPGDKMPKWRVILLNWCWFLMKRPGEDKVRPACQHKQRCS 365
 Db 306 LSVVVTVIYVYHHDPPGDKMPKWRVILLNWCWFLMKRPGEDKVRPACQHKQRCS 365
 QY 366 LASVMSAVAPPASNGNLLYIFRGDLGVHCVPPTDSGVVGVGRMACSPTHDEHLLHGGQ 425
 Db 366 LASVLSAGAGPPTSGNLLYIFRGDLGVHCVPPTDSGVVGVGRMACSPTHDEHLLHGGQ 425
 QY 426 PPEGDPDLAKILLEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFSVFTIICITIG 485
 Db 426 PEGDPPDLAKILLEVRYIANRRCODESEVICSEWKFACVVDPLCLMAFSVFTIICITIG 485
 QY 486 ILSAPNFEAVSKDFA 502
 Db 486 ILSAPNFEAVSKDFA 502
 RESULT 10
 QSUMH9 RAT PRELIMINARY; PRT; 531 AA.
 AC QSUMH9
 DT 01-FEB-2005 (TRENBLrel. 29, Created)
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Nicotinic acetylcholine receptor alpha 7 subunit splice variant 7-
 DE 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley;
 RX PubMed=1532233; DOI=10.1124/mol.104.000059;
 RA Severance E.G., Zhang H., Cruz Y., Pakhlevanians S., Hadley S.H.,
 RA Amin J., Wecker L., Reed C., Cuevas J.;
 RT "The alpha7 nicotinic acetylcholine receptor subunit exists in two
 RT isoforms that contribute to functional ligand-gated ion channels.";
 RL Mol. Pharmacol. 66:420-429(2004).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
 CC family.
 DR EMBL; AV671974; AAV31080.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045211; C:postsynaptic membrane; IEA.
 DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR006201; Neur_chan.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006029; Neur_chan memb.
 DR InterPro; IPR002394; Nic/ace receptor.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan memb; 1.
 DR PRINTS; PR00254; NICOTINIC.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.


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KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport. 88.6%; Pred. No. 2.3e-198;
SQ SEQUENCE 531 AA; 59746 MW; A8C67E0DE3EFDF47 CRC64;

Query Match 93.3%; Score 2522.5; DB 2; Length 531;
Best Local Similarity 88.6%; Pred. No. 2.3e-198;
Matches 466; Conservative 18; Mismatches 13; Indels 29; Gaps 1;

QY 6 GGWTLAALASLLHVSLOGSFQRLKYLKYNPNPLRPVANDSQPLTVYFSLSLQIMDV 65
D 6 GGTWLAALAAHLLHVSLOGSFQRLKYLKYNPNPLRPVANDSQPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNNIWLQMSWTHYLQWNSYEGVGVKTVRFPDQIWKPDILLYN----- 116
D 66 DEKNQVLTNNIWLQMSWTHYLQWNSYEGVGVKTVRFPDQIWKPDILLYN----- 116
QY 117 -----SADERPDATFHTNVLNVSNGHCQYLPPGIFKSSCYIDVRW 156
D 126 DLQNMLREACAQAGEDLRVSADERPDATFHTNVLNVSNGHCQYLPPGIFKSSCYIDVRW 185
QY 157 FPDVQVCHCKFGSWSYGGWLSLDLQWQADISGYIPNGEWDLVGIPGKRSRFPYECCKEP 216
D 186 FPDVQVCHCKFGSWSYGGWLSLDLQWQADISGYIPNGEWDLVGIPGKRSRFPYECCKEP 245
QY 217 YPDVTFTVMRRRTLYYGNLNLIPCVLIISALALLVFLPADSGEKLISGITVLLSLTTFM 276
D 246 YPDVTFTVMRRRTLYYGNLNLIPCVLIISALALLVFLPADSGEKLISGITVLLSLTTFM 305
QY 277 LLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVIVLYQHHDHDPGGMKPKWTRVILL 336
D 306 LLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVIVLYQHHDHDPGGMKPKWTRVILL 365
QY 337 NWCAMPFLMRKPGEDKVRPAQCHQKRCRCSLASVEMSAVAPPPASNGNLLIYIGRGLDGVH 396
D 366 NWCAMPFLMRKPGEDKVRPAQCHQKRCRCSLASVEMSAVAPPPASNGNLLIYIGRGLDGVH 425
QY 397 CVPTPDGSGVVCGRMACSPHDEHLHGGOPPGDPLAKILREVRVIANRFRQDESEAV 456
D 426 CAPTPDGSVVCGRMACSPHDEHLHGGOPPGDPLAKILREVRVIANRFRQDESEAV 485
QY 457 CSEWFAACVDRCLMAFSVFTIICITIGLMSAPNFVEAVSKDPA 502
D 486 CSEWFAACVDRCLMAFSVFTIICITIGLMSAPNFVEAVSKDPA 531

RESULT 11
ACHA7 CHICK STANDARD; PRT; 502 AA.
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 subunit precursor.
GN Name=CHRNA7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand S., Barak S., Ballivet M.,
RA Millar N., Valera S., Barnas T., Ballivet M.;
RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
RT developmentally regulated and forms a homo-oligomeric channel blocked
RT by alpha-BTX."
RL Neuron 5:847-856(1990).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519; DOI=10.1016/0896-6273(90)90031-A;

RA "Brain alpha-bungarotoxin binding protein cDNAs and MBAs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily."
RL Neuron 5:35-48(1990).
RN
RP NUCLEOTIDE SEQUENCE OF 1-18.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
RT promoter develops during morphogenesis of the central nervous
RT system."
RL EMBO J. 11:4529-4538(1992).
RN
RP PROTEIN SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
RA Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but
RT homologous proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN
RP MUTAGENESIS OF LEU-270.
RX MEDLINE=92049732; PubMed=1719423; DOI=10.1038/353846a0;
RA Rech F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
RA Husy N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal
RT nicotinic receptor."
RL Nature 353:846-849(1991).
RN
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829; DOI=10.1038/359500a0;
RA Galzi J.-L., Devillers-Thiery A., Husy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic."
RL Nature 359:500-505(1992).
CC
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in
CC the developing optic tectum between E5 and E16.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X68586; CAA48576.1; -; mRNA.
CC EMBL; X52295; CAA36543.1; -; mRNA.
CC EMBL; X68246; CAA48317.1; -; Genomic_DNA.
CC F01; JN0113; JN0113.
CC PDB; 1KL8; NMR; B=201-219.
CC PDB; 1KL8; NMR; B=201-219.
CC Ensemble; ENSGALG0000004096; Gallus gallus.
CC InterPro; IPR006029; Neur_chan_memb.
CC InterPro; IPR006201; Neur_chan_lig_bd.
CC InterPro; IPR002394; Nic/ace_receptor.
CC PANTHER; PTHR18945; Neur_chan; 1.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
```


DR	PRINTS; PRO0254; NICOTINTCR.	
DR	PRINTS; PRO0252; NRIONCHANNEL.	
DR	TIGRFAMS; TIGR00860; LIC; 1.	
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.	
KW	3D-structure; Direct protein sequencing; Glycoprotein; Ion transport;	
KW	ionic channel; Multigene family; Postsynaptic membrane; Signal;	
KW	Transmembrane; Transport.	
FT	SIGNAL 1 23	
FT	CHAIN 24 502	Neuronal acetylcholine receptor protein,
FT		alpha-7 subunit.
FT		Extracellular.
FT	TOPO_DOM 24 230	
FT	TRANSMEM 231 255	
FT	TRANSMEM 262 280	
FT	TRANSMEM 296 317	
FT	TOPO_DOM 318 469	
FT	TRANSMEM 470 490	
FT	CARBOHYD 46 46	
FT	CARBOHYD 90 90	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD 133 133	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID 150 164	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID 212 213	By similarity.
FT		Associated with receptor activation (By
FT		similarity).
FT	MUTAGEN 270 270	L->S;: Suppresses inhibition by the
FT		open-channel blocker QX-222.
SQ	SEQUENCE 502 AA; 56947 MW; 572325D4309AD2FD CRC64;	
Query Match		
Best Local Similarity 89.9%; Score 2429; DB 1; Length 502;		
Matches 449; Conservative 18; Mismatches 28; Indels 0; Gaps 0;		
QY	8 VMLAASLLHVSLOGEFORKLYKELVKNYNPLERPANDSPLTYVYFSLSLQIMQVDE 67	
DB	8 LMLAAGLVRESLQGEFORKLYKELVKNYNPLERPANDSPLTYVYFSLSLQIMQVDE 67	
QY	68 KQVLTNTIWLQSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLYNSADERFDATEH 127	
DB	68 KQVLTNTIWLQSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLYNSADERFDATEH 127	
QY	128 TNVLNSSGHCQYLPPIFKSCYIDVRWFPDVOHCKLKFGSWSGVGSWLDLQOEADI 187	
DB	128 TNVLNSSGHCQYLPPIFKSCYIDVRWFPDVOHCKLKFGSWSGVGSWLDLQOEADI 187	
QY	188 SGYIPNGEWDLVGIPKRSERYECCKEYPDVFTVTVMRRRTLYYGLNLLIPCVLISAL 247	
DB	188 SGYISNGEWDLVGIPKRTSEYECCKEYPDITFTVTVMRRRTLYYGLNLLIPCVLISAL 247	
QY	248 ALLVFLPADSGEKISLGTIVLLSTFTFMLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307	
DB	248 ALLVFLPADSGEKISLGTIVLLSTFTFMLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307	
QY	308 VVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHKQRCSLA 367	
DB	308 VVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHKQRCSLS 367	
QY	368 SVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLLHGQPP 427	
DB	368 SNEWTVSQCSNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDEHLLHGQPP 427	
QY	428 EGDPLAKILEVRYIANFRQDSREAVCSBWKFAACVDRICLMAFSVFTIITIGIL 487	
DB	428 EGDPLAKILEVRYIANFRQDSREAVCSBWKFAACVDRICLMAFSVFTIITIGIL 487	
QY	488 MSAPNFEAVSKDEFA 502	
DB	488 MSAPNFEAVSKDEFA 502	
RESULT 12		
ID	Q800C7 BRARE	
ID	Q800C7 BRARE PRELIMINARY; PRT; 509 AA.	
AC	Q800C7;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	

DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Nicotinic acetylcholine receptor alpha 7 subunit.	
GN	Name=chrna7;	
OS	Brachydanio rerio (zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]_SEQUENCE	
RP	NUCLEOTIDE SEQUENCE.	
RX	PubMed=14643683; DOI=10.1016/S1567-133X(03)00126-1;	
RA	Zirger J.M., Beattie C.E., McKay D.B., Thomas Boyd R.;	
RT	"Cloning and expression of zebrafish neuronal nicotinic acetylcholine	
RT	receptors";	
RL	Gene Expr. Patterns 3:747-754(2003).	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	
CC	-1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)	
CC	family.	
DR	EMBL; AY247962; AAO91913.1; -; mRNA.	
DR	HSSP; P22770; 1KL8.	
DR	Ensembl; ENSDARG0000022423; Danio rerio.	
DR	ZFIN; ZDB-GENE-040108-3; chrna7.	
DR	GO; GO:0016021; C: integral to membrane; IEA.	
DR	GO; GO:0045211; C: postsynaptic membrane; IEA.	
DR	GO; GO:0005230; F: extracellular ligand-gated ion channel acti. .; IEA.	
DR	GO; GO:0005216; F: ion channel activity; IEA.	
DR	GO; GO:0030594; F: neurotransmitter receptor activity; IEA.	
DR	GO; GO:0004889; F: nicotinic acetylcholine-activated cation-se. .; IEA.	
DR	GO; GO:0006811; F: ion transport; IEA.	
DR	InterPro; IPR006201; Neur_chan.	
DR	InterPro; IPR006202; Neur_chan_LBD.	
DR	InterPro; IPR006029; Neur_chan_memb.	
DR	InterPro; IPR002394; Nic/ace_receptor.	
DR	Pfam; PF02931; Neur_chan_LBD; 1.	
DR	Pfam; PF02932; Neur_chan_memb; 1.	
DR	PRINTS; PR00254; NICOTINIC.	
DR	PRINTS; PR00252; NRIONCHANNEL.	
DR	TIGRFAMs; TIGR00860; LIC; 1.	
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.	
KW	Ion transport; Ionic channel; Postsynaptic membrane; Receptor;	
KW	Transmembrane; Transport.	
SQ	SEQUENCE 509 AA; 58056 MW; 1BF152F4245578BA CRC64;	
Query Match		
Best Local Similarity 76.7%; Score 2073.5; DB 2; Length 509;		
Matches 386; Conservative 51; Mismatches 56; Indels 15; Gaps 5;		
QY	7 GWV-----LALAASLLHVSLOGEFORKLYKELVKNYNPLERPANDSPLTYVYFSLSLQ 61	
DB	2 GIWEYTLVFTTTCCLWSVSLQEQHQRLLYRLDMKDYNFLERFVFNDSHSLTYVYFSLSLQ 61	
QY	62 IMDVDEKQVLTNTIWLQSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLYNSADER 121	
DB	62 IMDVDEKQVLTNTIWLQSWTDHYLQNVSEYPGVKTVPDPGQIWKPDILLYNSADER 121	
QY	122 FDATHTNVLNSSGHCQYLPPIFKSCYIDVRWFPDVOHCKLKFGSWSGVGSWLDLQ 181	
DB	122 FDATHTNVLNSSGHCQYLPPIFKSCYIDVRWFPDVOHCKLKFGSWSGVGSWLDLQ 181	
QY	182 MOEADISGYIPNGEWDLVGIPKRSERYECCKEYPDVFTVTVMRRRTLYYGLNLLIPC 241	
DB	182 MIDADITGYIANGEDLVVEVFGRRNERFYDCCKEYPDVFTVTVMRRRTLYYGLNLLIPC 241	
QY	242 VLISALALLVFLPADSGEKISLGTIVLLSTFTFMLVAEIMPATSDSVPLIAQYFATM 301	
DB	242 VLISALALLVFLPADSGEKISLGTIVLLSTFTFMLVAEIMPATSDSVPLIAQYFATM 301	
QY	302 IIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHKQ 361	
DB	302 IIVGLSVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEDKVRPACQHKQ 361	
QY	362 RCCLSLASVEMSAVAPPPA--SNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDEH 419	

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Db 362 PRSSLSVDLN-ISPQVAQSTNGNLLYIGPRGMDTHIYATSPDGVICSRVLATGEEDV- 419
Qy 420 LLHGQGPPE-----GDDPLAKILEVRYIANRFRCDSEAVCSWKFAACVVDRLCLM 473
Db 420 LPGAQASSVSSSGPGGETELSKILDEVYISKFRDQDEBTVCNWKFAASVIDRLCLM 479
Qy 474 AFSVFTICTIGILMSAPNVEAVSKDF 501
Db 480 AFSFTILCTIGILMSAPNVEAISKDF 507

RESULT 13
Q6ZM45_BRARE
ID Q6ZM45_BRARE PRELIMINARY; PRT; 507 AA.
AC Q6ZM45;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Novel protein similar to mouse and rodent cholinergic receptor,
DE nicotinic, alpha polypeptide 7 (CHRNA7).
GN Name=chna7; Synonyms=OTDARP0000001918; ORFNames=dz70B1.1-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AL928677; CAE49579.1; -; Genomic DNA.
DR HSSP; P22770; 1KL8.
DR Ensembl; ENSDARG00000035785; Danio rerio.
DR ZFIN; ZDB-GENE-040108-3; Chrna7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0004889; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006029; Neu channel memb.
DR InterPro; IPR006202; Neu chan lig_bd.
DR InterPro; IPR006201; Neu channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00254; NICOTINICR.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane; Transport.
SQ SEQUENCE 507 AA; 57703 MW; 5CD57BC6FA4A3216 CRC64;

Query Match 75.7%; Score 2047.5; DB 2; Length 507;
Best Local Similarity 77.8%; Pred. No. 2.3e-159;
Matches 382; Conservative 49; Mismatches 47; Indels 13; Gaps 5;

Qy 19 VSLQGEFORLKYELVKNYPLRPVANDSPQITVYFSLQLQIMDVDEKNOVLTTNIWL 78
Db 20 VSLQGEHRRLYELDMKDYNPLRPVFNTHSITVYFSLQIMDVDEKNOVLTTNIWL 79
Qy 79 QMSWTDHYIOMNVSEYGVKTVRFPDQIWKPDILLYNSADRFDAFTFTNVLNVSSGHC 138
Db 80 QLYWYDYIQLWNASYEGVTNRFPDQIWKPDILLYNSADRFDAFTFTNVLNVSSGAC 139
Qy 139 QYLPPGIFKSSCYIDVRWPFVQHKLKEGWSYCGWSLDLQMQEADISGYIPNGEWDL 198
Db 140 QYLPPGIFKSTCYIDVRWPFVQHKLKEGWSYCGWSLDLQMQEADISGYIPNGEWDL 199

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Qy 199 VGIPGKRSERFVECCKEPYDPDTFTVTMRRTLYYGLNLLIPCVLISALALLVFLLPADS 258
Db 200 V---GRNERFYDCKCKEPYDPDTFTVTMRRTLYYGLNLLIPCVLISALALLVFLLPADS 256
Qy 259 GKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASWTMIIVGLSVVTVVLQYH 318
Db 257 GKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFATWTMIVGLSVIATVWLQYH 316
Qy 319 HHDPPGGKMPKWTIRVILLNWCWFLRMKRPGBDKVRPACOHKQRCCLASVEMSAVAPP 378
Db 317 YHDPGGKMPKWTIRVILLNWCWFLRMKRPGBDKVRPACCHNKPSSLSVDLN-ISPVG 375
Qy 379 A--SNGNLLYIGFRLDGVHCVPDPDGGVVCGRMACSPHDEHLLHGGQPE-----GD 430
Db 376 AQSTNGNLLYIGFRLDGVHCVPDPDGGVVCGRMACSPHDEHLLHGGQPE-----GD 434
Qy 431 PDLAKILEVRYIANRFRCDSEAVCSWKFAACVVDRLCLMAFVSFTICTIGILMSA 490
Db 435 TSLSKILDEVYISKFRDQDEBTVCNWKFAASVIDRLCLMAFSLFTILCTIGILMSA 494
Qy 491 PNFVEAVSKDF 501
Db 495 PNFVEAISKDF 505

RESULT 14
Q7T2R9_FUGRU
ID Q7T2R9_FUGRU PRELIMINARY; PRT; 513 AA.
AC Q7T2R9;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Nicotinic acetylcholine receptor alpha 8b subunit (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Tetraodontiformes;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE; 22859682; PubMed=13679024; DOI=10.1016/S0888-7543(03)00153-8;
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes."
RL Genomics 82:441-451(2003).
CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC family.
DR EMBL; AY299466; AAP58381.1; -; mRNA.
DR HSSP; P22770; 1KL8.
DR Ensembl; SINFRUG00000139100; Fugu rubripes.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045211; C:postsynaptic membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neu_chan_LBD.
DR InterPro; IPR006029; Neu channel memb.
DR InterPro; IPR002394; Nic/ace_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00254; NICOTINICR.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW Transport.
NON_TER 1
SQ SEQUENCE 513 AA; 57294 MW; 03315A831B0CA499 CRC64;

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Query Match		68.3%;	Score 1845;	DB 2;	Length 513;
Best Local Similarity		68.5%;	Pred. No. 1e-142;		
Matches 355;		Conservative 47;	Mismatches 74;	Indels 42;	Gaps 7;
QY	20	SLOGEFQRLKYLKELVQNYNPLERPVANDSQPLTVYFSLQLQIMVDKQNVLTNNIWLQ	79		
DB	1	SLOGEYQRLKYLKELVQNYNPLERPVANDSQPLTVYFSLQLQIMVDKQNVLTNNIWLQ	60		
QY	80	MSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLVNSADERFDATFHTNNVNSSGHQ	139		
DB	61	LYWTDIYLTWNPESYGVQNLRFPSQVWTPDILLVNSADERFDATFHTNNVNSAGY	120		
QY	140	YLPPIGFKSSCYIDVWFPPDVQCHKLKFGSMYSYGWSDLOQOEADISGYIPNGSWDLV	199		
DB	121	YIPPGILKSTCYIDVWFPPDVQCHKLKFGSMYSYGWSDLOQOEADISGYIPNGSWDLV	180		
QY	200	GIPGKSERFYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG	259		
DB	181	GVPKRNELYYDCKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG	240		
QY	260	EKISLGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVVIVLQYHH	319		
DB	241	EKISLGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVVIVLQYHH	300		
QY	320	HPDGGKMPKTRVILLNNCAWFLRMKPCGEDKVRPA--COR-KQRCCSLASVMSAV--	374		
DB	301	HPDGGKMPKTRVILLNNCAWFLRMKPCGEDKVRPA--COR-KQRCCSLASVMSAV--	360		
QY	375	-----APPASGNL--LVIGRGLDGVHCVTPDPSGVVC-GRMACSPHDDH	419		
DB	361	LSVPLAQTSGPSCPTGTSNGSMGFYSTVHTDSSSCPSPSDSGVALGRNHSPPSE--	418		
QY	420	LLHGGGPPG-----DPLAKTLEEVRYIANFRCODESEAVCSWKFA	463		
DB	419	----AEPVGGSGGSLGMGVRSVIPPPEIMCILIEVSYIAQFRDQDEAEICSEWKFA	474		
QY	464	ACVVDRLCLMAFVSFTIITCTIGILMSAPNFVEAVSKDF	501		
DB	475	AAVVDRLCLVAFLSFIITCTIGILMSAPNFVEAVSKDF	512		
RESULT 15					
ID	Q03481	CHICK PRELIMINARY;	PRT;	511	AA.
AC	Q03481				
DT	01-NOV-1996	(TrEMBLrel. 01, Created)			
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Alpha8 subunit of nicotinic acetylcholine receptor precursor.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Brain;				
RX	MEDLINE=90315158; PubMed=2369519; DOI=10.1016/0896-6273(90)90031-A;				
- RA	Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;				
RT	"Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal				
RT	subtypes of this branch of the ligand-gated ion channel gene				
RT	superfamily.";				
RL	Neuron 5:35-48(1990).				
- CC	-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).				
- CC	-I- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)				
CC	family.				
CC	EMBL; X52296; CAA36544.1; -; mRNA.				
DR	PIR;	JH0173;	JH0173.		
DR	HSSP;	P22770;	1KL8.		
DR	Ensembl;	ENSGALG00000015336;	Gallus gallus.		
DR	GO;	GO:0016021;	C:integral to membrane; IEA.		
DR	GO;	GO:0045211;	C:postsynaptic membrane; IEA.		
DR	GO;	GO:0005230;	F:extracellular ligand-gated ion channel acti. . .; IEA.		
DR	GO;	GO:0005216;	F:ion channel activity; IEA.		
DR	GO;	GO:0030594;	F:neurotransmitter receptor activity; IEA.		
DR	GO;	GO:0004889;	F:nicotinic acetylcholine-activated cation-se. . .; IEA.		
DR	GO;	GO:0006811;	P:ion transport; IEA.		
DR	InterPro;	IPR006201;	Neur_channel.		
DR	InterPro;	IPR006202;	Neur_chan_LBD.		
DR	InterPro;	IPR006029;	Neu_channel_memb.		
DR	InterPro;	IPR002394;	Nic/ace_receptor.		
DR	Pfam;	PF02931;	Neur_chan_LBD; 1.		
DR	Pfam;	PF02932;	Neur_chan_memb; 1.		
DR	PRINTS;	PRO0254;	NICOTINICR.		
DR	PRINTS;	PRO0252;	NRIONCHANNEL.		
DR	TIGRFAM;	TIGR00860;	LIC; 1.		
DR	PROSITE;	PS00236;	NEUROTR_ION_CHANNEL; 1.		
KW	Ion transport; Ionic channel; Postsynaptic membrane; Receptor; Signal;				
KW	Transmembrane; Transport.				
FT	SIGNAL	1	30	Potential.	
FT	CHAIN	31	511	Potential.	
SQ	SEQUENCE	511	AA;	58705	MW; 10F362D153EC87A7
					CRC64;
Query Match		67.2%;	Score 1816.5;	DB 2;	Length 511;
Best Local Similarity		68.8%;	Pred. No. 2.2e-140;		
Matches 342;		Conservative 56;	Mismatches 94;	Indels 5;	Gaps 4;
QY	8	VMLAASLLHVSLOGEFQRLKYLKELVQNYNPLERPVANDSQPLTVYFSLQLQIMVD	67		
DB	16	LWASLFLAFFKVSQGESQRLYRDLNLYNLERPVANDSQPIVVELQLSLQIIDVD	75		
QY	68	KNOVLTTNIWLQMSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLVNSADERFDATPH	127		
DB	76	KNOVLTTNAWLQMYWVDIYLSWDQYEGVQNLRFPSQIWPDPILLVNSADERFDATPH	135		
QY	128	TNVLVNSSGHCYLPPIGFKSSCYIDVWFPPDVQCHKLKFGSMYSYGWSDLOQOEAD	187		
DB	136	TNVLVNYSGCYIIPPGILKSTCYIDVWFPPDVQCHKLKFGSMYSYGWSDLOQOEAD	195		
QY	188	SGYIPNGSWDLVIGIPKSERFYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISAL	247		
DB	196	SNYISNGEWDLVGVFGKRNELYYECKEPPYDPDVTFTVMRRRTLYYGLNLLIPCVLISGL	255		
QY	248	ALLVFLPADSGEKISLGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVGLS	307		
DB	256	ALLVFLPADSGEKISLGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVGLS	315		
QY	308	VVTVVLVLYQHHDHPDGKMPKTRVILLNNCAWFLRMKPCGEDKVRP--ACQHK--QRR	364		
DB	316	VVTVVLVLYQHHDHPDGKMPKTRVILLNNCAWFLRMKPCGEDKVRP--ACQHK--QRR	374		
QY	365	SLASVMSAVAPPPASNGNLLYIGRGLDGVHCVTPDPSGVVCGRMACSPHDDHLLGG	424		
DB	375	SLKNTVMNVLPCHQPSNGNMIY-SYHTMENPCPNQNDLGSKSGKITCPLSEDNEHVQK	433		
QY	425	QPEGGDPLAKTLEEVRYIANFRCODESEAVCSWKFAACVVDRLCLMAFVSFTIICT	484		
DB	434	ALMDTIPVIVKILEVQFIAMFRKQDEGEITCSEWKFAAAVVDRLCLVAFLTFAICTF	493		
QY	485	GTLSAPNFVEAVSKDF	501		
DB	494	TILMSAPNFIEAVSKDF	510		
Search completed: March 28, 2006, 13:33:56					
Job time : 237 secs					